

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
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ROY, Paul H. ², 28 Charles Garnier, Loretteville,
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20 ¹:Canadian citizenship
 ²:American citizenship

25 (ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AND THEIR
 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND
 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEOAL, BACTERIAL,
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

35 (A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

40 (v) COMPUTER READABLE:

45 (A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

55 (vii) PRIOR APPLICATION DATA:

 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

	CAAACATCGTG	AGCACATCCT	TCTTTCTCGT	CAGGTAGGTG	TACCTTACAT	50
	CATCGTATTTC	TTAAACAAAT	GCGACCTTGT	TGATGACGAA	GAATTACTTG	100
20	AATTAGTAGA	AATGGAAGTA	CGTGAACCTTC	TTTCTACTTA	TGACTTCCC	150
	GGTGATGACA	CTCCAGTAAT	CCGTGGTTCA	GCTCTTGAG	CGCTTAACGG	200
	TGAAGCTGGT	CCTTACGGTG	AAGAACAGT	TCTTGCTCTT	GTAGCAGCAC	250
	TTGACTCTTA	CATCCCAGAG	CCAGAGCGTG	CAATCGACAA	AGCATTCTG	300
	ATGCCAACATCG	AAGACGTATT	CTCAATTCT	GGTCGTGGTA	CAGTAGTAAC	350
25	AGGCCGTGTT	GAAGCTGGTA	TCATCAAAGT	TGGTGAAGAA	GTAGAGATCG	400
	TTGGTATTAA	AGATAACAGT	AAAACAAC	TAAC	GGCGT	450
	CGTAAACTTC	TTGACGAAGG	CCGTGCAGGT	GAGAACTGTG	GTATCTTACT	500
	TCGTGGTACT	AAGCGTGAAG	AAGTACAACG	TGGTCAAGTA	CTTGCTAAAC	550
	CAGGTACAAT	CAAGCCGCAC	ACTAAATTG	ACCGAGAAGT	ATACGTACTT	600
30	TCTAAAGAAG	AAGGTGGTCG	TCACACTCCA	TTCTTAAATG	GTACC GTCC	650
	ACAGTTCTAC	TTCCGTACAA	CTGACGTAAC	TGGTGCRA	T CAGTTGAAAG	700
	AAGGC GTTGA	AATGGTAATG	CCAGGTGACA	ACGTTGAAAT	GTCAGTAGAA	750

35 2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

	CGGTGCGATC	CTCGTGGTCG	CCGCGACCGA	CGGCCCCCATG	GCCCCAGACCC	50
	GCGAGCACGT	CCTGCTCGCC	CGTCAGGTG	CGGTTCCCAC	CATCCTCATC	100
	GCCCTCAACA	AGTCCGACAT	GGTTGACGAC	GAGGAAATGA	TGGAAC	150
55	CGAGGAGGAG	TGCCGCGACC	TGCTGGAGTC	CCAGGACTTC	GATCGCGATG	200
	CCCCGATCGT	CCAGGTTTCC	GCTCTGAAGG	CCCTCGAGGG	CGACGCGGAG	250
	TGGGTTGCCA	AGATCGAGGA	GCTCATGGAG	GCTGTGGATT	CCTACATCCC	300
	CACCCCCGAG	CGCGATATGG	ACAAGCCCTT	CCTCATGCCG	ATCGAGGACG	350
	TCTTCACGAT	CACAGGTGCGT	GGCACGGTCG	TCACGGGGCG	TGTTGAGCGT	400
60	GGCAAGCTGC	CGATCAA	CTCGAGGTGAG	ATCCTCGGTA	TCCGTGATCC	450

	CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG	500
	AGGCATGGC CGCGAGAAC TGTGGCCTGC TGCTGCGCG TACCAAGCGC	550
	GATGAGGTTG AGCGCGGCCA GGTTGTGGCC ATTCCCAGGCT CCATCACGCC	600
5	TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAC GAAGAGGGCG	650
	GCCGTACCAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT	700
	ACCACGGACG TGACCGGGCGT CATCACCCCTC CCCGAGGGCA CCGACATGGT	750
	CATGCCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG	800
	CCATGGAGCC CGGCTGGGCT TCGCCA	826

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2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

	TGGTGCATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC	50
	GTGAGCACAT CCTTTAGCT GGCCAAATCG GTGTTCTGC ATTCTGAGTA	100
30	TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACCTAC CCAGGTGACG	200
	ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA	250
	GCTCAAGAACG CTAAAATCAT GGAATTAAATG GAAGCTGTAG ACTCTTACAT	300
	TCCAGAACCA GAACGTGACA ACGACAAACC ATTCACTGATG CCAATTGAGG	350
35	ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA	400
	CGTGGTGAAG TTCTGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA	450
	ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTC CGTAAAAACT	500
	TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT	550
	CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT	600
40	CACTCCACAT ACTAAATTAA AAGCGCAAGT TTACGTTTA TCTAAAGAAC	650
	AAGGTGGACG TCATACACCA TTCTTAACCA ACTACCGTCC ACAATTCTAC	700
	TTCGGTACTA CTGACATTAC TGGTGTATAC ACTTTACCGAG AAGACGTAGC	750
	TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCAAC	800
	CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC	835

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2) INFORMATION FOR SEQ ID NO: 4

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
denitrificans

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG TCGGCCGCTG ACGGCCGAT GCCGAAACAG CGCGAACACA	50
	TCCTGCTGAG CCGCCAGGTT GGCGTGCCT ACATCATCGT CTTCTGAAC	100
	AAGGCCGACA TGGTTGACGA CGCCGAGCTG CTTGAGCTGG TGAAATGGA	150
	AGTCGCGAR CTGCTGAGCA AGTACGACTT CCCGGGCGAC GACACCCGA	200
	TCGTGAAGGG TTCGGCCAAG CTGGCGCTGG AAGGCACAA GGGCGAAGTC	250
10	GGCGAACAGG CCATCATGGC GCTGGCCGCT GCGCTGGACT CGTACATCCC	300
	GACGCCTGAG CGTGCCTGTT ACGGCGCGTT CCTGATGCCG GTTGAAGACG	350
	TGTTCTCGAT CTCGGGTCGC GGCACCGTGG TGACCGGCCG TATCGAACGC	400
	GGCATCATCA AGGTGGCGA GGAAATCGAA ATCGTCGGTC TGGTGCCGAC	450
	GGTGAAGACG ACCTGCACGG GCGTGGAAAT GTTCCGCAAG CTGCTGGACC	500
15	AAGGTCAAGC CGCGACAAAC GTGGGCATCC TRCTGCGCG CACCAAGCGT	550
	GAAGACGTCC AGCGCGGCCA GGTTCTGGCC AAGCCGGCT CGATCACCCC	600
	GCACACGGAC TTCACGTCCG AGGTGTACAT CCTGTCCAAG GAAGAAGGCG	650
	GCCGTCACAC TCCGTTCTTC CAAGGCTATC GTCCCCAGTT CTACTTCCGC	700
	ACGACGGACG TGACGGGCAC GATCGAGCTG CCGGCCGACA AGGAAATGGT	750
20	CCTGCCGGGC GACAACGTGG CCATGACGGT CAAGCTGCTG GCTCCGATCG	800
	CCATGGAAGA AGGCCTGCGT TCGCCAC	827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 35 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Anaerorhabdus furcosus*
 - (B) STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC CTAGTAGTTG CTGCAACTGA TGGACCAATG CCTCAAACTC	50
	GTGAACATAT CTTACTTGCT CGTCAAGTAG GTGTTCCAAG AATGGTTGTA	100
	TTCTTGAACA AATGCGACAT GGTTGAAGAT GAAGAATTAA TCGACCTTGT	150
	TGAAATGGAA GTTCGTGAAC TTCTAAGTGC TTACGGTTTC GAAGGTGATG	200
45	ATACACCACT TATCCGTGGT TCTGCATTA AATCTCTTGA AGGAAATGCT	250
	GATTGGGAAG CAAAAGTTGC TGAATTAAATG GATGCAGTTG ACTCTTGGAT	300
	TCCAACCTCA ACTCATGAAA CAGACAAACCC ATTCTTAATG GCTGTTGAAG	350
	ATGTATTCAAC AATTACAGGT CGTGGTACAG TTGCTACTGG ACGTGTTGAA	400
	CGTGGACACT TAAACCTTAA CGAAGAAGTT GAAATCGTTG GTATTCAATG	450
50	TACTAAAGAAA TCAGTTGTTA CTGGTATCGA AATGTTCCGT AAATTATTAG	500
	ACTATGCTGA AGCAGGAGAC AACATTGGTG CATTATTACG TGGTGTTCCT	550
	CGTGATGAAA TCGAACGTGG ACAATGTCTA GCTAACCTG GATCAGTTAC	600
	TCCACATACA GCTTTCAAAG CTCAAAGTATA CGTATTAACG AAAGAAGAAG	650
	GTGGACGTCA TACACCATTC GTAACTAAC ACCGTCCTCA ATTCTATTTC	700
55	CGTACAACCTG ACGTAACAGG AGTTGTTAAA CTTCTGAAAG GTACTGAAAT	750
	GGTTATGCCT GGAGACAAACA TCGAAATGAT CGTTGAATTA ATCGCTCCAA	800
	TCGCTGTTGA ACAAGGAACG AAG	823

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 5 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACTC	50
GTGAGCACAT	CCTTCTTCT	CGTCAAGTAG	GTGTACCTTA	CATCGTTGTA	100
TTCTTAAACA	AATGCGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
20 AGAAATGGAA	GTTCGCGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
ACATTCCGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400
25 CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
AGAAAATGCT	TCTACAACTG	TAACCTGGTGT	AGAGATGTTTC	CGTAAACTTC	500
TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
30 AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAAG	AAGGTACTGA	750
AATGGTAATG	CCTGGTGACA	ACATCGAAAT	GACTATCGAA	CTTATCGCTC	800
CAATCGCTAT	CGAAGAGGGA	ACTAA			825

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2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACAC	50
GTGAGCACAT	CCTTCTTCT	CGTCAAGTAG	GTGTACCTTA	CATCGTTGTA	100
55 TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAATTAT	TAGAATTAGT	150
AGAAATGGAA	GTTCGCGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
ACATTCCGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
60 ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400

	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAATGCT	TCTACAAC TG	TAACTGGTGT	AGAGATGTT C	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
5	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATTGAAAT	GACTATCGAA	CTTATCGCTC	800
	CAATCGCTAT	CGAAGAGGGA	ACTAAATT C			829

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2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
- (B) STRAIN: ATCC 8503

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

30	CGGTGCTATC	ATCGTAGTTG	CTGCTACTGA	TGGTCCTATG	CCTCAAAC TC	50
	GCGAGCACAT	CCTTTGGCT	CGTCAGGTAA	ACGTTCCGAG	ATTGGTTGTA	100
	TTCATGAACA	AGTGTGACAT	GGTTGACGAC	GAGGAATGT	TGGAATTGGT	150
	TGAGATGGAG	ATGAGAGAGT	TGCTTCATT	CTATCAATT C	GACGGTGACA	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTTG	GTGCATTGAA	CGGTGATGCT	250
	CAATGGGAAG	ATAAAGTAAT	GGAGTTGATG	GAAGCTTGTG	ATACTTGGAT	300
35	TCCTCTGCCT	CCGCGCGAAA	TCGACAAGCC	GTTCTTGATG	CCGGTTGAGG	350
	ACGTATTCTC	AATCACGGGT	CGTGGTACTG	TTGCTACAGG	TCGTATCGAG	400
	ACAGGTATTG	TTAAGGTTGG	TGAGGAAGTT	CAGATCATCG	GTCTTGGCGC	450
	TGCTGGTAAG	AAATCTGTTG	TTACAGGTGT	TGAGATGTT C	CGTAAGTTAT	500
	TGGATCAAGG	TGAGGCTGGT	GATAACGTTG	GTTTGTGCT	TCGCGGTATC	550
40	GATAAGAATG	AGATCAAGCG	TGGTATGGTA	ATCTGCCACC	CGGGTCAGGT	600
	TAAAGAGCAT	TCTAAGTTCA	AGGCTGAGGT	TTATATCTTG	AAGAAAGAGG	650
	AAGGTGGTCG	TCACACTCCG	TTCCACAACA	AAATATCGTCC	TCAGTTCTAT	700
	ATCCGTACAT	TGGATGTAAC	TGGTGAGATC	ACTTTGCCGG	AAGGAACTGTA	750
	AATGGTAATG	CCGGGTGATA	ACGTAACGAT	CGAGGTTGAG	TTGATCTATC	800
45	CGGTAGCATG	TAGCGTAG				818

2) INFORMATION FOR SEQ ID NO: 9

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG	50
	TGTACCATACT ATCGTTGTT TCTTAAACAA AATGGATATG GTTGATGACG	100
	AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA	150
	TATGACTTCC CAGGCCACGA TGTTCTGTG ATCGCTGGTT CTGCTTTGAA	200
	AGCTCTTGAA GGCGATGCTT CATA CGAAGA AAAAATCATG GAATTAATGG	250
10	CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA	300
	TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT	350
	TGCTACAGGC CGTGTGAAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG	400
	AAATCGTTGG TATTGCTGAA GAAAATGCTA AAACAACATGT AACTGGTGT	450
	GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG	500
15	TGCATTGCTA CGTGGTGTG CTCGTGAAGA CATCCAACGT GGACAAGTAT	550
	TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTAA AGCTGAAGTT	600
	TACGTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA	639

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2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: CSG 197

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

5	GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT	50
	CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG	100
	AAATGGAAGT TCGTGA CTTAAGCGAAT ATGACTTCCC AGGTGACGAT	150
40	GTACCTGTAA TCTCTGGTTC TGCATTA AAAA GCTTTAGAAG GCGACGCTGA	200
	CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC	250
	CAACACCCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC	300
	GTATTCTCAA TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG	350
	TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG	400
45	AATCAAGCAA AACAACTGTT ACTGGTGTAG AAAATGTTCCG TAAATTATTA	450
	GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTC	500
	ACGTGATGAC GTACAACGTG GTCAAGTTT AGCTGCTCCT GGTACTATTA	550
	CACCAACATAC AAAATTCAA GCGGATGTTT ACGTTTTATC TAAAGATGAA	600
	GGTGGTCGTC ATACACCA CTTCACTAAC TACCGCCCCAC AATTCTATT	650
50	CCGTACTACT GACGTAACGT GTGTTGTTAA CTTACCAGAA GG	692

2) INFORMATION FOR SEQ ID NO: 11

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC ATCGTTGTG CTGCAACTGA TGGTCCGATG CCTCAAACTC GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA TTCTGAACA AATGCGATAT GGTAGACGAC GAAGAAATGT TGGAACTCGT TGAAATGGAA ATGAGAGAAC TCCTTCATT CTATGATTT GATGGTGACA	50 100 150 200
15	ATACTCCTAT CATCCGTGGT TCTGCTCTG GCGCATTGAA CGGTGTTGAA AAATGGGAAG ACAAAAGTTAT GGAACTGATG GATGCAGTTG ATAACGGAT TCCACTGCCT CCGCGCGATG TTGATAAAACC ATTCTTGATG CCGGTTGAAAG ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA	250 300 350 400
20	ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCTTG GTTAGGTGA AGATAAGAAA TCAGTTGAA CTGGTGTGA AATGTTCCGT AAACGTGTTGG ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTGCTTCG TGGTATTGAC	450 500 550
25	AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAACCCAG GTCAGATTAA ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAAG AAAGAAGAAG GTGGTCGTCA CACTCCGTTCA CACAACAAAT ACCGTCCTCA GTTCTACTTG CGTACTATGG ACTGTACAGG TGAAATCACT TTGCCGGAAG GAACAGAAAT	600 650 700 750
	GGTAATGCCG GGTGATAACG TAACTATTAC AGTTGAGTTG ATTTACCCAG TAGCATTGAA CCCGGGCTTC G	800 821

30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCAGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC GTGAGCATAT TCTTCTTGCC CGTCAGGTG GTGTTCCAGC GATTGTTGTT TTTCTTAATA AGGTTGATCA GTTGTATGAT GCTGAGCTTT TGGAGCTTGT TGAGCTTGAA GTTCCGGAGT TATTGTCGAA ATATGATTT CCAGGAGACG	50 100 150 200
50	ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAAGAT AAAAGCATTG GTGAAGATGC GTTCTGCTTT TTGATGAGTG AAGTTGATAA TTATATACCG ACGCCTGAAAC GTCCCTGTTGA TCAGCCGTTT TTGATGCCAA TTGAAGATGT TTTTTCGATT TCGGGTCTG GAACCTGTTGT GACGGGTCGT	250 300 350 400
55	GTTGAGCGTG GTGTTATTAA GTTGGTGAA GAAGTTGAGA TTATCGGCAT TCGTCCAAGT TCTAAGACAA CAGTTACAGG GTTGAATG TTCCGCAAGC TTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTGGCGA AGCCTGCTTC	450 500 550 600
60	GGTTACACCT CATACTGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG ATGAAGGTGG TCGTCATACT CCATTTTCA CGAATTATCG TCCTCAGTTT TATTTCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC	650 700 750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG	800
TTCCAATTGC CATGGAAGAA AAACCTCGTT TTGCTATC	838

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2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
- (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC	CTTGTGTTGG	CCGCCACCGA	CGGCCCGATG	GCTCAGACCC	50
GCGAGCACGT	GCTGCTCGCT	CGTCAGGTGG	GCGTCCCGAA	GATCCTCGTC	100
GCTCTGAACA	AGTGCATAT	GGTCGACGAC	GACGAGCTCA	TCGAGCTCGT	150
25 TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAATGGCTTC	GATCGCGATT	200
GCCC GGTCAT	CCACGTGTC	GCTTACGGCG	CACTGCACGA	TGACGCTCCG	250
GACCACGAGA	AGTGGGTTGA	GCAGATCAAG	AAGCTCATGG	ACGCCGTCGA	300
TGACTACATC	CCGACCCCGG	TCCACGATCT	GGACAAGCCG	TTCCCTGATGC	350
CGATCGAAGA	TGTCTTCACC	ATCTCCGGCC	GTGGCACCGT	GGTGACCGGC	400
30 CGTGTGAGC	GTGGTAAGCT	CCCGGTCAAC	TCCAACGTCG	AGATCGTCGG	450
CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
AGCAGATGGA	CGAGTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
GGCATCAAACC	GTGACCAAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
35 AGGACGAAGG	CGGCCGTAC	TCGCCGTTCT	TCTCCAACTA	CCGTCCGCAG	700
TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
- (B) STRAIN: ATCC 27534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCGATG	GCTCAGACCC	50
GCGAGCACGT	GCTGCTCGCT	CGTCAGGTGG	GCGTGCCGCG	TATCCTCGTC	100
60 GCCCTGAACA	AGTGCATAT	GGTCGACGAC	GAAGAGCTCA	TCGAGCTCGT	150

	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAACGGCTTC	GATCGCGATT	200
	GCCCCGTAT	CCACACCTCC	GCCTACGGCG	CGCTGCACGA	TGACGCTCCG	250
	GACCACGACA	AGTGGGTTGA	GTCCGTCAAG	GAACTCATGA	AGGCCGTCGA	300
5	CGAGTACATC	CCGACCCGA	CCCACGATCT	GGACAAGCCG	TTCCTGATGC	350
	CGATCGAAGA	TGTGTTCAC	ATCTCCGGC	GTGGCACCGT	GGTTACCGGC	400
	CGTGTGAGC	GTGGTAAGCT	CCCGGTCAAC	TCCAACGTTG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
10	GGCATCAACC	GTGACCAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTAC	TCGCCGTTCT	TCTCCAACTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
15	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

2) INFORMATION FOR SEQ ID NO: 15

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 838 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
 - (B) STRAIN: S2308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

35	TGGCGCGATC	CTGGTGGTTT	CGGCTGCTGA	CGGCCCGATG	CCGCAGACCC	50
	GCGAGCACAT	CCTGCTTGCC	CGTCAGGTTG	GGTTCGGCGC	GATCGTCGTG	100
	TTCCTCAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTGCGCGAAC	TTCTGTCGAA	GTACGAATTG	CCCGGCGACG	200
	AAATCCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCC	250
40	AAGGAACTGG	GCGAAGATGC	CATCCGCAAC	CTGATGGACG	CGGTTGACAG	300
	CTACATTCCG	ACCCCGGAAC	GCCCGATCGA	CCAGCCGTT	CTGATGCCGA	350
	TCGAAGACGT	GTTCTCGATC	TCCGGCCGTG	GTACGGTTGT	GACGGGTCGC	400
	GTGTGAGCGCG	GTATCGTAA	GGTCGGTGAA	GAAGITGAAA	TGGTGGCAT	450
	CAAGGCAGC	ACGAAGACCA	CGGTTACCGG	CGTTGAAATG	TTCCGCAAGC	500
45	TGCTCGACCA	GGGCCAGGCT	GGCGACAAAC	TTGGCGCGCT	GATCCGCGGC	550
	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTTC	600
	TGTGAAGCCG	CACACCAAGT	TTAAGGCAGA	AGCCTATATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTCA	CCAACCTACCG	TCCGCAGTTTC	700
	TACTTCCGTA	CGACGGACGT	GACGGGTGTT	GTGACGCTTC	CGGCTGGCAC	750
50	GGAAATGGTC	ATGCCTGGCG	ATAACGTCGC	CATGGACGTT	ACCCCTGATCG	800
	TGCCGATCGC	CATGGAAGAG	AAGCTTCGCT	TCGCTATC		838

2) INFORMATION FOR SEQ ID NO: 16

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 771 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
 (B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC GGCCCGATGC CGCAAACGCG TGAGCACATC CTGCTGGCGC GTCAGGTTGG CGTTCGTAC ATCATCGTGT TCCTGAACAA GTGCGACATG GTGGACGACG CCGAACTGCT CGAGCTGGTC GAGATGGAAG TTGCGAACT CCTGTCGAAG TACGACTTCC CGGGCGACGA CACGCCGATC GTGAAGGGTT CGGCGAAGCT GGCGCTGGAA GGCGACACGG GCGAGCTGGG CGAAGTGGCG 15 ATCATGAGCC TGGCCGACGC GCTGGACACG TACATCCCAG CGCCGGAGCG TGCAGTTGAC GGCGCGTTCC TGATGCCGGT GGAAGACGTG TTCTCGATCT CGGGCCGCGG TACGGTGGTG ACGGGTCGTG TCGAGCGCGG CATCGTGAAG GTCGGCGAAG AAATCGAAAT CGTCGGTATC AAGCCGACGG TGAAGACGAC CTGCAACGGC GTTAAATGT TCCGCAAGCT GCTGGACCAA GGTCAAGCAG 20 GCGACAACGT TGGTATCCTG CTGCGCGGCA CGAACGCGTA AGACGTGGAG CGTGGCCAGG TTCTGGCGAA GCCGGGTTCG ATCACGCCGC ACACGCACCTT CACGGCTGAA GTGTACGTGC TGAGCAAGGA CGAAGGCGGC CGTCACACGC CGTTCTTCAA CAACTACCCT CGCGAGTTCT ACTTCCGTAC GACGGACGTG 25 ACGGGCTCGA TCGAGCTGCC GAAGGACAAG GAAATGGTGA TGCCGGCGA CAACGTGTCG ATCACGGTGA A	50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 771
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2) INFORMATION FOR SEQ ID NO: 17

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 829 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
35	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG TGAGCACATC CTGCTGGTC GTCAGGTTGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGTGACG AAGAGCTGCT GGAAGCTGGTA GAAATGGAAG TTCGTGAACT TCTGTCCCAG TACGACTTCC CGGGCGACGA TAATCCAATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GCGGAAGCAG 50 AGTGGGAAGC TAAAATCGTT GAGCTGGCTG GCTACCTGGA TTCTTACATC CCTGAGCCAG AGCGTGTAT CGATAAGCCG TTCCCTGCTGC CAATCGAAGA CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT ACTGCGAAAT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 55 CGAAGGCCGT GCTGGTGAGA ACGTTGGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCAGG CTCTATCAAG CCACACACCA AGTTCGAATC TGAAGTGTAC ATCCCTGTCCA AAGACGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC GTACAACGTGA CGTGACCGGC ACCATCGAAC TGCCAGAAGG CGTTGAGATG 60 GTAATGCCTG GCGACAACAT CAAAATGGTT GTTACCCCTGA TCCACCAAT	50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800
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CGCGATGGAT GACGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
- (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20	CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG	50
	AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCTTACAT CATCGTGTTC	100
	CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA	150
25	AATGGAAGTT CGTGAACCTC TGTCTCAGTA CGACTTCCCG GGCGATGACA	200
	CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAACAGCAG	250
	TGGGAAGCTA AAATYGTGTA GCTGGCTGGC TTCTGGATT CCTACATCCC	300
	AGAACCCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG	350
	TATTCTCCAT CTCCGGCCGT GGTACCCTG TTACCGGTCG TGTAGAGCGC	400
30	GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATA	450
	TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG	500
	AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT	550
	GAAGAAATCG AACGTGGTCA GGTTCTGGCT AAGCCAGGCT CTATCAAGCC	600
	GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGGCG	650
	GCCGTACATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT	700
35	ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT	750
	AATGCCAGGC GACAACATCA AAATGGTTGT TACCTGATC CACCCAATCG	800
	CGATGGACGA CGGTCTGCGT TTCTG	824

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2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- 45 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Cedecea lapagei</i>
	(B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG	50
AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCTTACAT CATCGTGTTC	100
CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA	150
60 AATGGAAGTT CGTGAACCTC TGTCTCAGTA CGACTTCCCA GGCGATGATA	200

	CCCCAATCAT	CCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAACGCAGAG	250
	TGGGAAGCTA	AAATCGTTGA	GCTGGCTGGC	TTCCTGGATT	CCTACATCCC	300
	AGAACCCAGTA	CGTGCAATCG	ACCTGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
5	TATTCTCCAT	CTCCGGCCGT	GGTACCGTTG	TKACCGGTCG	TGTAGAGCGC	400
	GGTATCGTTA	AAGTGGGCGA	AGAAGTAGAA	ATCGTTGGTA	TCAAAGATAAC	450
	TGCGAAATCT	ACCTGTACTG	GCGTTGAAAT	GTTCCCGAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCCGTGG	TATCAAACGT	550
	GAAGAAATCG	AACGTGGTCA	GGTTCTGGCT	AAGCCAGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGTACAT	CCTGTCCAAA	GACGAAGGCG	650
10	GCCGTACATAC	TCCGTTCTTC	AARGGTACC	GTCCACAGTT	CTACTTCCGT	700
	ACCACTGACG	TGACCCGGTAC	CATCGAACTG	CCAGAAGGCG	TAGAGATGGT	750
	AATGCCAGGT	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

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2) INFORMATION FOR SEQ ID NO: 20

- (i) SEQUENCE CHARACTERISTICS:
- | | | |
|----|-----|----------------------|
| 20 | (A) | LENGTH: 831 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | |
|-----|---------------------------------------|
| (A) | ORGANISM: <i>Chlamydia pneumoniae</i> |
| (B) | STRAIN: CWL 029 |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

	GC GGAGCTAT	CCTAGTCGTT	TCAGCTACAG	ACGGAGCTAT	GCCACAAACT	50
	AAAGAACATA	TCTTGCTAGC	TCGCCAGGTT	GGAGTTCCCTT	ATATCGTTGT	100
35	TTTCTTGAAT	AAAGTAGATA	TGATCTCTCA	AGAAGATGCT	GAACCTTATTG	150
	ACCTGTTGA	GATGGAACCTT	AGTGAGCTTC	TTGAAGAAAA	AGGCTACAAA	200
	GGATGCCCTA	TTATCCGTGG	TTCTGCTTTG	AAAGCTCTTG	AAGGTGATGC	250
	AAATTATATC	GAAAAAGTTC	GAGAACTTAT	GCAAGCTGTG	GATGACAACA	300
	TCCCTACACC	AGAAAAGAGAA	ATTGATAAGC	CTTTCTTAAT	GCCTATCGAA	350
40	GACGTATTCT	CAATCTCTGG	TCGTGGTACT	GTGGTTACAG	GAAGAATCGA	400
	GC GTGGAATC	GT TAAAGTTT	CTGATAAAAGT	TCAGCTCGTG	GGATTAGGAG	450
	AGACTAAAGA	AA CAATCGTT	ACTGGAGTCG	AA ATGTTCA G	GA AAGAACTT	500
	CCTGAAGGTC	GTG CAGGAGA	AA AC GTTGGT	TT ACTCCTCA	GAGGTATTGG	550
45	AA AGAACGAT	GT TGAAGAG	GT ATGGTGGT	TT GT CAGCCT	AA CAGCGTGA	600
	AGCCTCATAAC	GA AA ATT TAAG	TCAGCTTTT	AC GTTCTTC A	GA AAGAAGAA	650
	GGCGGACGTC	AT AAG CCTTT	CTT CAGCGGA	TACAGACCTC	AG TTCTTCTT	700
	CCGTACTACA	GAC GTGACAG	GAGTCGTAAC	TCTT C CTGAA	GGAACTGAAA	750
	TGGTAATGCC	TGGAGATAAC	GT TGAGCTTG	AT GTTGAGCT	CATTGGAACA	800
50	GTTGCTCTTG	AAGAAGGAAT	GAGATTGCA	A		831

2) INFORMATION FOR SEQ ID NO: 21

- 55 (i) SEQUENCE CHARACTERISTICS:
- | | |
|-----|----------------------|
| (A) | LENGTH: 826 bases |
| (B) | TYPE: Nucleic acid |
| (C) | STRANDEDNESS: Double |
| (D) | TOPOLOGY: Linear |

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCATG CCTCAGACCA	50
AAGAACATAT TCTTTGGCG AGACAGGTTG GTGTTCTTA CATCGTTGTT	100
10 TTCCTTAACA AAATCGATAT GATTCTCAA GAAGATGCTG AGCTCGTAGA	150
CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GTTATAAAAG	200
GTTGCCAAT TATCCGTGGT TCTGCTTGA AAGCCTTAGA AGGTGATGCA	250
AGCTACGTTG AAAAAATTG CGAGTTAATG CAAGCAGTGG ATGATAACAT	300
CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG	350
15 ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACgtATCGAG	400
CGTGGAATCG TTAAAGTGGG TGATAAAAGTA CAGATTGTTG GTTAAGAGA	450
TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTCAGA AAAGAACTTC	500
CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT	550
AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA	600
20 ATCTCACACA CAATTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG	650
GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC	700
CGTACAACAG ATGTTACAGG TGTTGTAACT CTCCCAGAAG GTACAGAGAT	750
GGTTATGCCA GGCGATAACG TTGAATTGCA AGTTCAATTAA ATTAGCCCAG	800
TAGCTCTAGA AGAAGGTATG AGATT	826

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2) INFORMATION FOR SEQ ID NO: 22

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 822 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

45	GGGGCTATT TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACCAA	50
	AGAGCATATT CTTTTGGCAA GACAAGTTGG GTTCTCTTAC ATCGTTGTTT	100
	TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC	150
	TTGGTTGAGA TGGAGTTGGC TGAGCTCTT GAAGAGAAAAG GATACAAAGG	200
	GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTGGAA GGGGATGCTG	250
	CATACATAGA GAAAGTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC	300
50	CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA	350
	CGTGTCTCT ATCTCCGGAC GAGGAACGTG AGTAACCTGGA CGTATTGAGC	400
	GTGGAATTGT TAAAGTTCC GATAAAAGTTC AGTTGGTCGG TCTTAGAGAT	450
	ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTCAGAA AAGAACTCCC	500
	AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA	550
55	AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCAAA CAGTGTAAA	600
	CCTCATACAC GGTTTAAGTG TGCTGTTAC GTTCTGCAA AAGAAGAAGG	650
	TGGACGACAT AAGCCTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC	700
	GTACAAACAGA CGTTACAGGT GTGGTAAACTC TGCCCTGAGGG AGTTGAGATG	750
	GTCATGCCTG GGGATAACGT TGAGTTGAA GTGCAGTTGA TTAGCCCTGT	800
60	GGCTTAGAA GAAGGTATGA GA	822

2) INFORMATION FOR SEQ ID NO: 23

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAAC TA	50
	GAGAACACAT CCTACTTG CCGTCAGGTAA ACGTACCTAG AATTGTTGTG	100
	TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAAATTGT TAGAGCTTGT	150
	TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA	200
25	ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTAA CGGTGATGCT	250
	AAGTGGGTAG CTACTGTAGA AGCTCTAAATG GATGCTGTTG ATACTTGGAT	300
	CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCCTTATG CCAATCGAAG	350
	ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG	400
	GCTGGTGTAA TCAACACAGG TGATCCCTGTT GACATCGTAG GTATGGGTGA	450
30	CGAGAAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC	500
	TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT	550
	GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCAAGT	600
	TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG	650
35	AAGGTGGACG TCACACTCCA TTCCACAAACA AATACCGTCC TCAGTTCTAT	700
	GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAAG AAGGTGTAGA	750
	AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC	800
	CAATCGCTCT TAACGAGGGT CTTAGATTG CGATC	835

40 2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55	CGGC CGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG CGGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT	150
	AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CGGGCGACG	200
60	ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGC GACGCA	250

	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCC	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCAG	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
5	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCCAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCWCCATCAA	600
10	GCCGCACACC	ATGTTGAAT	CYGAAGTGT	CATCCTGTCC	AAAGACGAAG	650
	GC GCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTTGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGG				816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
- (B) STRAIN: ATCC 43162

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

	CGCGATCCTG	GTTGTTGCTG	CAACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACACATCCT	GCTGGGTCGY	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTC	100
35	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	AATGGAAGTT	CGTGAACCTC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAWGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCTGGC	TTCCTGGATT	CTTACATCCC	300
	GGAACCAAGAG	CGTGCAGATTG	ACAAGCCGTT	CCTGCTGCC	ATCGAAGACG	350
40	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAARGACAC	450
	TGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAGCGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCT	CTATCAAGCC	600
45	GCACACCAAG	TTCGAATCTG	AA GTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTACATAC	TCCGTTCTTC	AARGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGTAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAAACATCA	AAATGGTTGT	TACCCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGC			825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACCTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCAG	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGT	CATYCTGTCY	AAAGATGAAG	650
	CGGGCCGTCA	TACTCCGTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

25

2) INFORMATION FOR SEQ ID NO: 27

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAACCTGC	TGTCTCAGTA	CGATTTCGG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCCCTGGATT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCATTG	ACAAGCCGT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCGCAAA	CTGCTGGACG	500
55	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTT	TGCTGCGTGG	TATCAAACGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTCGAATCTG	AAAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTACATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTT	TTGAGATGGT	750
60	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCCTGATC	CACCCGATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Citrobacter freundii*
- (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT GCTGCGACTG ACGGCCGAT GCCGCAGACT CGTGAGCACA	50
	TCCTGCTGGG TCGTCAGGTA GGC GTTCCGT ACATCATCGT GTTCCTGAAC	100
	AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGA ACTGG TAGAAATGGA	150
	AGTCGTGAA CTTCTGTCTC AGTACGATT CCCGGGCGAC GACACTCCGA	200
	TCGTTCTGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGAAGC AGAGTGGGAA	250
25	GCGAAAATCA TCGAACTGGC TGGCTTCCGT GATTCTTACA TCCCAGAAC	300
	AGAGCGTGCAG ATTGACAAGC CGTTCTGCT GCCTATCGAA GACGTATTCT	350
	CCATCTCCGG TCGTGGTACC GTTGT TACCG GTCGTGTTAGA GCGCGGTATC	400
	ATCAAAGTTG GTGAAGAAAGT TGAAATCGTT GGTATCAAAG AGACTGCTAA	450
	GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC	500
30	GTGCTGGTGA GAACGTTGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA	550
	ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCTCTATCA AGCCGCACAC	600
	CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGACGAA GCGGGCCGTC	650
	ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT	700
	GACGTGACTG GTACCATCGA ACTGCCGAA GGC GTAGAGA TGGTAATGCC	750
35	GGCGACAAAC ATCAAATGG TTGTTACCCCT GATCCACCCA ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Citrobacter sedlakii*
- (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGCGCGATC CTGGTTGTTG CCGCGACTGA CGGCCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGT A CATCATCGT	100
	TTCCTGAACA AATGCGACAT GGTTGATGAC GAAAGAGCTGC TGGAACTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG	200
	ACACGCCGAT CGTTCTGTGG TCAGCTCTGA AAGCGCTGGA AGGCGACGCA	250
60	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCGTG ATTCTTACAT	300

	TCCGGAACCA GAGCGTGCAG	TTGACAAGCC GTTCCTGCTG CCGATCGAAG	350
	ACGTATTCTC CATCTCCGGT	CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTGGG	CGAAGAAAGTT GAAATCGTT GTATCAAAGA	450
	GACTGCGAAG TCTACCTGTA	CTGGCGTTGA AATGTTCCGC AAACGTCTGG	500
5	ACGAAGGCCG TGCGGGTGAG	AACGTAGGTG TTCTGCTGCG TGGTATCAA	550
	CGTGAAGAAA TCGAACGTGG	TCAGGTACTG GCGAAGCCGG GCACCATCAA	600
	GCCGCCACACC AAGTTCGAAT	CTGAAGTGT A TATTCTGTCC AAAGATGAAG	650
	GCAGGCCGTCA TACTCCGTTC	TTCAAAGGCT ACCGTCCGCA GTTCTACTTC	700
	CGTACAACGT ACGTGACTGG	CACCATCGAA CTGCCGGAAG GCGTAGAGAT	750
10	GGTAATGCCG GGCACAAACA	TCAAATGGT TGTTACCTG ATCCACCCGA	800
	TCGCGATGGA CGACGGTCTG	CGTTTC	826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- 20 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
- (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG TTGTTGCTGC	GACTGACGGC CCGATGCCGC AGACTCGTGA	50
	GCACATCCTG CTGGGTCGTC	AGGTAGGCCT TCCGTACATC ATCGTGTTC	100
	TGAACAAATG CGACATGGTT	GATGACGAAG AGCTGCTGGA ACTGGTAGAA	150
	ATGGAAGTTC GTGAACTTCT	GTCTCAGTAC GATTTCGGG GCGACGACAC	200
35	TCCGATCGTT CGTGGTTCTG	CTCTGAAAGC GCTGGAAGGC GAAGCAGAGT	250
	GGGAAGCGAA AATCATCGAA	CTGGCTGGCT TTCTGGATT TTACATCCG	300
	GAACCAGAGC GTGCGATTGA	CAAGCCGTT CAAGCTRCCTA TCGAAGACGT	350
	ATTCTCCATC TCCGGTCGTG	GTACCGTTGT TACCGGTCGT GTAGAGCGCG	400
	GTATCATCAA AGTTGGTGAA	GAAGTTGAAA TCGTTGGTAT CAAAGACACC	450
40	GCTAAGTCTA CCTGTACCGG	CGTTGAAATG TTCCGCAAC TGCTGGACGA	500
	AGGCCGTGCT GGTGAGAACG	TTGGTGTCT GCTGCGTGGT ATCAAACGTG	550
	AAGAAATCGA ACCTGGTCAG	GTACTGGCTA AGCCGGGCTC TATCAAGCCG	600
	CACACCAAGT TCGAATCTGA	AGTGTACATC CTGTCAAAG ACGAAGGC	650
45	CCGTCATACT CCGTTCTCA	AAGGCTACCG TCCGCAGTTC TACTTCCGTA	700
	CTACTGACGT GACTGGTACC	ATCGAACTGC CGGAAGGC GT AGAGATGGTA	750
	ATGCCGGCG ACAACATYAA	AATGGTTGTT ACYCTGATCC ACCCGATCGC	800
	GATGGACGAC GGTCTGCGTT	TCG	823

50 2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- 55 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
TGAGCACATC	CTGCTGGTC	GTCAGGTAGG	CGTTCCTGAC	ATCATCGTGT	100
TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTA	150
10 GAAATGGAAG	TTCGTGAAC	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
TACGCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAACGAG	250
AGTGGGAAGC	GAAAATCATC	GAACCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAC	400
15 GCGGTATCAT	CAAAGTTGGT	GAAGAAAGTTG	AAATCGTTGG	TATCAAAGAG	450
ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCCT	GGTATCAAAC	550
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAACGCCGG	CTCTATCAAG	600
CCGCACACCA	AGTTCGAAC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20 CGGCCGTCA	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
CGCGATGGAT	GACGGTCTGC	GTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

CGGAGCTATA	TTAGTTGTT	CAGCAGCTGA	TGGTCCAATG	CCTAAACAA	50
GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45 TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACCTTC	CCAGGAGACG	200
AYATTCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAAC	250
GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
CTACATCCC	ACACCAAGAAA	GAGCAACAGA	TAAGCCATT	TTAATGCCAG	350
50 TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTCAGAA	500
AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
GGTATCCAAA	GAACGTGAYAT	CGAAAGAGGT	CAAGTTTAG	CTCAAGTTGG	600
55 AACAACTAAC	CCACACAAAAA	AATTCGTAGG	TCAAGTATAC	GTACTTAAA	650
AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TCGATGGATA	CAGACCACAA	700
TTCTACTTCA	GAACAAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTGCTAT	C	841

60

2) INFORMATION FOR SEQ ID NO: 33

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

15 (A) ORGANISM: *Comamonas acidovorans*
 (B) STRAIN: ATCC 15668

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

20	CGGCGCCATC CTGGTGTGCT CGGCCGCTGA CGGCCCATG CCCAGACCC	50
	GCGAGCACAT CCTGCTGGCC CGTCAGGTGG CGGTGCCCTA CATCATCGTG	100
	TTCCTGAACA AGTGCACAT GGTGGACGAC GAAGAGCTGC TGGAACTGGT	150
	CGAAATGGAA GTGCGCGAGC TGCTTGCCAA GTACGACTTC CCCGGCGACG	200
	ACACCCCCAT CATCCCGGGC TCGGCCAAGC TGGCCCTGGA AGGCGACCAAG	250
25	TCCGACAAGG GCGAACCTGC CATCCTGCGC CTGGCTGAAG CACTGGACTC	300
	CTACATCCCC ACGCCCAGGC GCGCTGTGGA CGGCGCCTTT GCAATGCCCG	350
	TGGAAGACGT GTTCTCGATC TCTGGCCGTG GCACCGTGGT GACTGGCCGT	400
	ATCGAGCGCG GCATCATCAA GGTCGGCGAA GAAATCGAAA TCGTCGGTAT	450
	CCGCGACACC CAGAAGACCA TCGTCACCGG CGTGGAAATG TTCCGCAAGC	500
	TGCTGGACCA AGGTCAAGCT GGCGACAAACG TGGGTCTGCT GCTGCGCGGC	550
30	ACCAAGCGTG AAGACGTGGA ACGCGGCCAA GTGCTGTGCA AGCCCGGCTC	600
	CATCAAGCCC CACACCCACT TCACGGCTGA GGTGTACGTG CTGTCCAAGG	650
	ACGAAGGTGG TCGCCACACT CCGTTCTTCA ACAACTACCG TCCCCAGTTC	700
	TATTTCGTA CGACCGACGT GACCGGCTCC ATCGAGCTGC CCGCCGACAA	750
	GGAAATGGTG ATGCCTGGCG ACAACGTGTC GATCACCGTC AAGCTGATCG	800
35	CCCCCATCGC CATGGAAGAA GG	822

2) INFORMATION FOR SEQ ID NO: 34

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC CGTGAGCACG TCCTCCTGGC CCGTCAGGTG GGTGTGCCCT	50
	ACATCCTCGT CGCCCTCAAC AAGTGCACG TGTCGACGA CGAGGACCTC	100
	ATCGAGCTCG TCGAGATGGA GGTCCGTGAG CTCCCTGCCG AGCAGGACTA	150
	CGACGAGGAC GCCCCGATCA TCCACATCTC CGCCCTCAAG GCCCTCGAGG	200
	GTGACCCGGA GTGGACCGAG CGCATCGTC ACCTCATGAA GGCCTGCGAC	250
60	GACGCCATCC CGGATCCGGA GCGCGAGACG GACAAGCCGT TCCTCATGCC	300

	GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC	350
	GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT	400
	ATCTCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA	450
5	CAAGTTCCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC	500
	GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG	550
	GGCGCCTACA CGCCGCACAC CGAGTCGAG GGCTCCGTGT ACATCCTCTC	600
	CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTCGACAAAC TACCGTCCGC	650
	AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG	700
	GG	702

10

2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium cervicis*
- (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

30	GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGCAGTCCGA	50
	CGATCCTGGT TGCCCTAAC AAGGCCATA TGTCGACGA TGAGGAAATG	100
	CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT	150
	CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG	200
	GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC	250
35	ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC	300
	GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC	350
	GTGTTGAGCG TGGCAAGCTC CCGATCAAAT CTGAGGTTGA AATCCTCGGT	400
	ATCCCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA	450
	GTCCATGGAT GAAGCATGGG CAGGCAGGAA CTGTGGTCTC CTCCCTGCGTG	500
40	GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTGTC CGTTCCCGBT	550
	TCGATCACCC CGCACACCAA CTTCACCGGA CAGGTCTACA TCCTCAAGAA	600
	GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAACTAC CGTCCCGAGT	650
	TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC	689

45

2) INFORMATION FOR SEQ ID NO: 36

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium flavescens*
- (B) STRAIN: ATCC 10340

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

	GGTTGTTGCT	GCAACCGATG	GTCCTATGCC	GCAGACCCGC	GAGCACGTT	50
	TTCTGGCTCG	CCAGGTTGGC	GTTCCTTACA	TCCTCGTTGC	TCTTAACAAG	100
	TGCGACATGG	TTGATGATGA	GGAAATCATC	GAGCTCGTTG	AGATGGAAAT	150
5	CCCGAAGACTG	CTCGCTGAGC	AGGACTACGA	CGAGGATGCC	CCCATCATCC	200
	ACATCTCCGC	TCTCAAGGCT	CTTGAGGGTG	ACGAGAAGTG	GGTACAGGCC	250
	ATCGTCGACC	TCATGCAGGC	CTGCGATGAC	TCCATTCCGG	ATCCGGAGCG	300
	CGAGACCGAC	AAGCCCTTCC	TCATGCCTAT	CGAGGACATC	TTCACCATCA	350
	CCGGCCGCGG	TACCGTTGTT	ACCGGCCGTG	TTGAGCGTGG	CGTTTGAAAG	400
10	GTCAACGAGG	ATGTTGAGAT	CATCGGCATC	AAGGAGAAGT	CCATCTCCAC	450
	CACCGTTACC	GGTATCGAAA	TGTTCCGCAA	GATGATGGAC	TACACCGAGG	500
	CTGGCGACAA	CTGTGGTCTG	CTTCTGCGTG	GTACCAAGCG	TGAAGAGGTC	550
	GAGCGCGGCC	AGGTTGTTAT	CAAGCCGGGC	GCCTACACCC	CCCACACCAA	600
	GTTCGAGGGT	TCCGTCTACG	TCCTCAAGAA	GGAAGAGGGC	GGCCGCCACA	650
15	CCCCGTTCAT	GGACAACATAC	CGTCCGCACT	TCTACTTCCG	TACCACTGAC	700
	GTGACCGGCG	TTGTTCACCT	GCCTGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACGTT	GATATGACCG	TTGAGCTCAT	CCAGCCCGTC	GCTAGGATGA	800
	GGGC					804

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium kutscheri*
- (B) STRAIN: ATCC 15677

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

	TGCCTCAGAC	CCGTGAGCAC	GTTCTTCTTG	CTCGCCAGGT	TGGCGTTCC	50
	TACATCCTCG	TTGCTCTTAA	CAAGTGGCAC	ATGGTTGACG	ATGAGGAAAT	100
40	CATCGAGCTC	GTTGAGATGG	AAGTTCGCGA	GCTTCTTGCT	GAGCAGGAGT	150
	ACGATGAAGA	GGCTCCAATC	ATCCACATCT	CTGCTTTGAA	GGCTCTTGAG	200
	GGCGACGAGA	AGTGGACTCA	GGCCATCATC	GACCTCATGC	AGGCTTGTGA	250
	TGACTCCATC	CCAGATCCAG	AGCGTGAGAC	CGACAAGCCA	TTCCCTCATGC	300
	CTATCGAGGA	TATCTTCACC	ATCACCGGTC	GTGGCACCGT	TGTTACCGGT	350
45	CGTGTGAGC	GCGGTTCCCTT	GAAGGTGAAT	GAGGACGTGG	AGATCATCGG	400
	CATCAAGGAG	AAGTCCACCA	CTACTACCGT	TACCGGTATC	GAAATGTTCC	450
	GTAAGCTTCT	TGATTACACC	GAAGCTGGCG	ATAACTGTGG	TCTGCTTCTT	500
	CGTGGTATCA	AGCGCGAAGA	CGTTGAGCGT	GGTCAGGTTG	TTGTTAACGCC	550
50	AGGCCTTAC	ACACCTCACA	CCGAGTTCGA	GGGCTCTGTT	TACGTTCTTT	600
	CCAAGGACGA	GGGCGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAAC	TGACGTTACC	GGTGTGTTGA	AG	692

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium minutissimum*
 (B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

10	CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACCG CGCGAGCACG TTCTTCTGGC CCGCCAGGTT GGCGTTCGT ACATCCTCGT TGCAGTGAAAC AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG	50 100 150 200
15	TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGGCACAG TCCATCGTT ACCTGATGCA GGCTTGCATG GACTCCATCC CGGATCCGGAA GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG	250 300 350 400
20	AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCCCGCACAC	500 550 600 650
25	CAAGTTCGAG GGTTCCGTCT ACGTCCTGAA GAAGGAAGAG GGCAGGCCGCC ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCAACC GACGTCACCG GTGTACCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA	700 750 797

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium mycetoides*
 (B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

45	GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT ACATCCTCGT TGCCTGAAAC AAGTGCACA TGTTGATGA TGAGGAGATC ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGGCG AGCAGGACTA CGACGAGGAC GCCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG	50 100 150 200
50	GCGACGGAGAA GTGGGTTCAAG TCCGTGCTCG ACCTCATGCA GGCGTGCAC GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACAGAGTCGA GATCATCGGC	250 300 350 400
55	ATCCCGACAA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA CAAGCTGCTC GATAACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG GGCAGCTACA CCCCCCACAC CAAGTTCGAG GTTCCGTCT ACGTCCGTGTC	450 500 550 600
60	CAAGGACGAG GGCAGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC AGTTCTACTT CCGCACCAACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG GG	650 700 702

2) INFORMATION FOR SEQ ID NO: 40

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
- (B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTGCCAGG TTGGCGTTCC TTACATCCTC GTTGCCTGA ACAAGTGCAGA	50
	CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG	100
	AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC	150
	TCCGCTCTGA AGGCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT	200
	TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA	250
25	CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC	300
	CGCGGTACCG TTGTTACCGG CGGTGTTGAG CGTGGCCGTC TGAACGTCAA	350
	CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG	400
	TTACCGGTAT CGAGATGTT CGCAAGATGA TGGACTACAC CGAGGCTGGC	450
	GACAACGTG GTCTGCTTCT GCCTGGTACCG AAGCGTGAGG ACGTTGAGCG	500
30	TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG	550
	AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGGCCG CCACACCCCG	600
	TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC	650
	CGGTGTTGTT CACCTGCCAG AGGG	674

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2) INFORMATION FOR SEQ ID NO: 41

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
- (B) STRAIN: ATCC 19412

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

	TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCCTTCCT	50
	TACATCCTCG TTGCACTGAA CAAGTGCAGAC ATGGTCGACG ACGAAGAAAT	100
55	CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT	150
	ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC	200
	GGCGAGCAGA AGTGGGTTGA CTCCCATCGTC GAACTGATGG AAGCTTGCAGA	250
	CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCCACCA TTCCGTATGC	300
	CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC	350
60	CGTGTGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG	400

	TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC	450
	GCAAGATGCT GGAECTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC	500
	CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC	550
5	AGGCGCTTAC ACCCCTCACT CTGAGTTCGA GGGCTCTGTC TACGTCCTGT	600
	CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA	650
	CAGTTCTACT TCCGCACCAC CGACGTGACC GGCAGTTGTGC ACCT	694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
- (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC CGCGAGCACG TTCTGCTGGC TCGCCAGGTT GGCAGTCCCT	50
	ACATCCTSGT TGCACTGAAC AAGTGCGACA TGGTTGACGA TGAGGARCTC	100
	CTSGAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA	150
	CGACGGAGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG	200
30	GCGACCSAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCAC	250
	GAGTCCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC	300
	GATTGAGGAC ATCTTCACCA TTACCGGTG CGGYACCGTT GTTACCGGCC	350
	GTGTTGAGCG TGGCDTCCTG AACGTSAACG ACGASGTTGA GATCATGGGY	400
	ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA	450
35	CAAGMTGMTG GACWCCGCAG AGGCTGGCGA CAACGCTGSW CTGCTGCTGC	500
	GTGGGTMSTA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG	550
	GGCGCKTACA CCCCGCACAC CGAGTTCGAG GGCTCCGTCT ACGTCCCTGTC	600
	CAAGGACGAG GGCGGGCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC	650
40	AGTTCTACTT CCGCACCACCG GACGTSACCG GTGTTGT	687

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*
- (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

60	CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT	50
	TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCCTCGTT GCACTGAACA	100

	AGTGCACAT GGTTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG	150
	GTCCCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT	200
	CCCGATCTCC GCACTGGCG CCCTGGACGG CGATCAGAAG TGGGTCGACT	250
5	CCATCCTCGA GCTCATGAAG GCTTGCACG AGTCATCCC GGACCCGGAG	300
	CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT	350
	TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTTGAGCGT GGCCTCCTGA	400
	ACCTGAACGA CGAGGTCGAG ATCCTGGCA TCCCGAGAA GTCCACCAAG	450
	ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA	500
	GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG	550
10	TCGAGCGAGG CCAGATCATC GCTAACCGG GCGCTTACAC CCCGCACACC	600
	GAGTTGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA	650
	CACCCCGTTC TTCGACAAC ACCGTCGCA GTTCTACTTC CGTACCAACG	700
	ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTACATGCCG	750
	GGCGACAAACG TTGAGATGAG CGTCAAGC	778

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2) INFORMATION FOR SEQ ID NO: 44

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium xerosis*
- (B) STRAIN: ATCC 373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

	CGCAGACCCG TGAGCACGTC CTCCGGCCC GCCAGGTCGG CGTCCCCCTAC	50
35	ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT	100
	CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG	150
	ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGCGC CCTCAATGGC	200
	GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA	250
	GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTG CTGATGCCG	300
40	TCGAGGACAT CTTCACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCCG	350
	GTGGAGCGCG GCACCCCTGAA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT	400
	CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA	450
	AGCTGCTGGA CTCCGCGAG GCGGGCGACA ACTGTGGCCT GCTGCTCCGC	500
45	GGCATCAAGC GCGAGGACAT CGAGCGCGC CAGATCATCG CGAAGCCGGG	550
	CGCCTACACC CCGCACACCG AGTTGAGGG CTCCGTCTAC ATCCCTGGCCA	600
	AGGACCGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAACTA CCGTCCGCAG	650
	TTCTACTTCC GCACCAACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG	700
	CAC	703

50

2) INFORMATION FOR SEQ ID NO: 45

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

	GGAGCGATAT	TGGTGGTGAG	CGCAGCGGAC	GGCCCGATGC	CGCAAACGCG	50
	GGAACACATT	GTATTGGCGA	AGCAAGTGGG	TGTTCCGAAC	ATAGTGGTTT	100
10	ACTTGAACAA	AGCGGACATG	GTGGATGACA	AAGAGCTGTT	GGAATTAGTG	150
	GAAATGGAAG	TGAGGGATT	ATTGAACAGT	TATGATTTC	CTGGGGATGA	200
	GACGCCATA	ATAGTGGGGT	CAGCGTTAAA	GGCGTTAGAA	GGTGACAAAGA	250
	GTGAGGTTGG	GGAGCCATCG	ATAATCAAAT	TAGTGGAAAC	GATGGACACG	300
	TACTTCCCAC	AGCCGGAGCG	AGCGATAGAC	AAACCGTTT	TAATGCCGAT	350
15	CGAACAGATGTG	TTTCGATAT	CGGGCCGAGG	GACGGTGGTG	ACGGGACGCG	400
	TAGAGCGAGG	GATCATAAA	GTGGGCGACG	AGATAGAGAT	TGTGGGGATC	450
	AAGGACACGA	CGAACAGAC	GTGCACGGGC	GTTGAGATGT	TTCGCAAATT	500
	ATTGGATGAA	GGTCAAGCGG	GTGACAACGT	AGGAATTTTA	TTGAGAGGGA	550
	CGAAACGCGA	AGAAGTGGAG	CGTGGTCAAG	TATTGGCGAA	ACCGGGATCG	600
20	ATCACGCCAC	ACAAGAAATT	TGAGGGCGAG	ATTTATGTGT	TGTCAAGGA	650
	AGAAGGGGGA	CGCCACACAC	CGTTTTACA	AGGCTATCGA	CCGCAATT	700
	ATTTCGCGAC	GACGGACGTG	ACGGGCCAGT	TATTGAGTTT	ACCGGAGGGG	750
	ATAGAGATGG	TGATGCCGGG	AGATAACGTG	AAAGTGACGG	TTGAATTGAT	800
	TGCGCCGGTA	GCGATGGATG	AAGGGCTACG	AT		832
25						

2) INFORMATION FOR SEQ ID NO: 46

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 816 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GCCAGGTAGG	CGTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAGATCATC	GAACCTGGCTG	AAACGCTGGA	CTCCTACATT	300
50	CCGGAACCTG	AGCGTACAT	CGACAAGCCG	TTCCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCA	ATCTCTGGTC	GTTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTAGG	TATCAAGCCG	450
	ACCACCAAGA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTTG	TCTGCTGCGT	GGTACCAAGC	550
55	GTGACCAAAT	CGAACGTGGT	CAGGTACTGG	CTAACGCCGG	CACCATCACT	600
	CCGCACACCA	AGTCGAATC	AGAAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGTTA	CCGTCCGCA	TTCTACTTCC	700
	GTACCACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAAACAT	CAAGATGGTT	GTTACCCCTGA	TCCACCCGAT	800
60	CGCCATGGAC	GATGGT				816

2) INFORMATION FOR SEQ ID NO: 47

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20	GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG	50
	TGAGCACATC CTGTTGGTC GCCAGGTAGG CGTTCGTAC ATCATCGTGT	100
	TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT	150
	GAGATGGAAG TTCCGGAACT GCTGTCAG TACGACTTCC CGGGCGACGA	200
	CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCAGAGCCG	250
25	AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACCTCTGGA CTCCTACATC	300
	CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA	350
	CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC	400
	GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG	450
	ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA	500
30	CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAACG	550
	GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT	600
	CCGCACACCA AGTTCGAACAT TGAAGTGTAC ATCCTGAGCA AGGATGAAGG	650
	CGGCCGTCACT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC	700
	GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG	750
35	GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCCTGA TCCACCCGAT	800
	CGCCATGGAC GATGGTCTGC G	821

40 2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- 45 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
- (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55	CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCATG CCTCAGACTC	50
	GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCTA CATCCTCGTA	100
	TTCATGAACA AATGCGACAT GGTAGATGAT GCCGAGCTGC TTGAGTTGGT	150
	TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG	200
60	ACTGCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC	250

	GGTTACAAAG AAAAAATCTT CGAACTAGCT GCTGCTTG GG ATAGCTACAT	300
	CCCCACTCCT CAACGTGCTG TAGACAAACC CTTCCTGTT CGGATCGAAG	350
	ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCAG TCGTAGAG	400
5	CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTT GTCTGAAGCC	450
	CACTCAGAAA ACTACCTGTA CTGGCGTGG AATGTTCCGC AAACGTCTGG	500
	ACGAAGGTCA GGCGGGTGAC AACGTAGGCG TACTGCTGCG CGGTACCAAA	550
	CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC	600
	TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG	650
	GTGGTCGTCA CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC	700
10	CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT	750
	GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA	800
	TTGCTATGGA AGAAGGTCTG CGCTTTGCGA	830

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2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
- (B) STRAIN: ATCC 13048

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG	50
	TGAGCACATC CTGCTGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT	100
	TCCTGAACAA ATGCGACATG GTTGTGACG AAGAGCTGCT GGAACCTGGTT	150
35	GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCG CGGGCGACGA	200
	CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCACGCGAG	250
	AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGAA TTCTTACATC	300
	CCRGAACCAG AGCGTGCAG TGACAAGCCG TTCCCTGCTGC CGATCGAAGA	350
	CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC	400
40	GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC	450
	ACCGCGAAAA CCACCTGTAC TGGCGTGAA ATGTTCCGCA AACTGCTGGA	500
	CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC	550
	GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG	600
	CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG	650
45	CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC	700
	GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG	750
	GTAATGCCGG GCGACAAACAT CAAAATGGTT GTTACCCCTGA TCCACCCGAT	800
	CGCGATGG	808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCGATG CCGCAGACTC	50
10	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT	150
	TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG	200
	ATACTCCGAT CGTTCTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCW	250
	GAGTGGGAAG CGAAAATCAT CGARCTGGCT GGCCACCTGG ATACCTATAT	300
15	CCCAGAACCA GAGCGTGCAG TTGACAAGCC GTTCTGCTG CCGATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGCGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TYAAAGTGGG CGAAGAAGTT GAAATCGTT GTATCAAAGA	450
	TACYCGAAA TCAACCTGTA CCGGCGTTGA AATGTTCCGC AAACGTCTGG	500
	ACGAAGGCCG TGCTGGTGAG AACGTTGGT TTCTGCTGCG TGGTATCAA	550
20	CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA	600
	GCCGCACACC AAGTCGAAT CTGAAGTGTAA CATTCTGTCC AAAGATGAAG	650
	GCGGTCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCSCA GTTCTACTTC	700
	CGTACAAC TGACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT	750
	GGTAATGCCG GGCGACAAACA TCAAAATGGT TGTTACCTG ATCCACCCGA	800
	TCGCGATGGA CGACGGTCTG CGTTCGCA	828

25

2) INFORMATION FOR SEQ ID NO: 51

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 825 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

45	TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGCCCTATG CCACAGACGC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCCTA CATCATCGTG	100
	TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT	150
	AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG	200
	ACACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA	250
	GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTTACAT	300
50	CCCAGAACCA GAACGTGCTA TCGATAAGCC ATTCTGCTG CCAATCGAAG	350
	ACGTATTCTC TATCTCCGGC CGTGGTACTG TTGTAACCGG TCGTGTAGAG	400
	CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTT GTATCAAAGA	450
	GACTGCTAAG TCTACCTGTA CTGGCGTGTGA AATGTTCCGC AAACGTCTGG	500
	ACGAAGGCCG TGCTGGTGAG AACGTTGGT TTCTGCTGCG TGTTATCAA	550
55	CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCAG GCTCAATCAA	600
	GCCGCACACC AAATTCGAAT CTGAAGTTA TATTCTGTCC AAAGATGAAG	650
	GCGGCCGTCA TACTCCGTT TCTAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAAC TGACGTGACCGG CACCATCGAA CTGCCGAGAAG GCGTAGAGAT	750
	GGTAATGCCA GGCGACAAACA TTCAGATGGT TGTTACCTG ATCCACCCAA	800
60	TCGCGATGGA TGACGGTCTG CGTTT	825

2) INFORMATION FOR SEQ ID NO: 52

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCCTT CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG	200
	ATACTCCAAT CGTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250
25	GAGTGGGAAG CGAAAATCAT CGAACCTGGCT GGCTTCCTGG ATTCTTACAT	300
	CCCAGAACCA GAGCGTGCAG TTGACAAGCC ATTCCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACGTGCTGG	500
30	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAA	550
	CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA	600
	GCCACACACC AAGTTCGAAT CTGAAGTGTG CATCCTGTCC AAAGACGAAG	650
	GC GGCGGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAAC TG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT	750
35	GGTAATGCCA GGCGACAAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA	800
	TCGCGATGGA CGACGGTCTG CG	822

40 2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- 45 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
- (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCCTA CATCATCGTG	100
	TTCCTGAACA AGTGCACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT	150
	AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCAGGGCGACG	200
60	ACACTCCAAT CGTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT	250

	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAG	TTGACAAGCC	ATTCCCTGCTG	CCAATCGAAG	350
5	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGCKAAA	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAA	550
	CGCGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
10	GCCACACACC	AAGTTCGAAT	CTGAAGTGT	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACGCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 25
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Enterobacter cloacae*
 - (B) STRAIN: ATCC 13047

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

	GATCCTGGTA	GTAGCTGCAG	CTGACGGCCC	AATGCCTCAG	ACTCGTGAGC	50
	ACATCCTGCT	GGGTCGTCA	GTAGGCGTTC	CTTACATCAT	CGTGTTCCTG	100
35	AACAAATGCG	ACATGGTTGA	TGACGAAGAG	CTGCTGGAAC	TGGTAGAGAT	150
	GGAAGTTCGT	GAACGTCTGT	CTCAGTACGA	TTTCCCAGGC	GACGATAACCC	200
	CAATCGTTG	TGGTTCTGCT	CTGAAAGCGC	TGGAAGGGCGA	CGCAGAGTGG	250
	GAAGMGAAAA	TCATCGAACT	GGCTGGCTAC	CTGGATTCTT	ACATCCCAGA	300
	ACCAGAGCGT	GCGATTGAYA	AGCCATTCT	GCTGCCAATC	GAAGACGTAT	350
40	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	CCGGTCGTGT	AGAGCGCGGT	400
	ATCATCAAAG	TGGGTGAAGA	AGTTGAAATC	GTTGGTATCA	AAGAGACTGC	450
	GAAGTCTACC	TGTACTGGCG	TTGAAATGTT	CCGCAAAC TG	CTGGACGAAAG	500
	GCCGTGCTGG	TGAGAACGTT	GGTGTCTGC	TGCGTGGTAT	CAAACGTGAA	550
	GAAATCGAAC	GTGGTCAGGT	TCTGGCGAAG	CCAGGCTCAA	TCAAGCCACA	600
45	CACCAAGTTC	GAATCTGAAG	TGTACATCCT	GTCCAAAGAC	GAAGGCGGCC	650
	GTCATACTCC	GTTCTTCAAA	GGCTACCGTC	CACAGTTCTA	CTTCCGTACA	700
	ACTGACGTGA	CCGGTACCAT	CGAACTGCCA	GAAGGCGTAG	AGGGTGGTAAT	750
	GCCAGGGCGAC	AACATCAAGA	TGGTTGTGAC	TCTGATCCAC	CCAATCGCGA	800
	TGGACG					806

50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

- 55
- (A) LENGTH: 826 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGTA	CATCATCGTG	100
10	TTCCTGAACA	AGTGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACCCCGAT	CGTTCGCGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAAACTGGCT	GGCCACCTGG	ATACCTAYAT	300
	CCCAGAACCA	GAGCGTGCAG	TTGACAAAGCC	GTTCCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATTTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCGAAA	ACCACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGGTGA	CATCCTGTCC	AAAGACGAAAG	650
	GCGGCCGTCA	CACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAAACA	TCAAGATGGT	TGTTACCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

25

2) INFORMATION FOR SEQ ID NO: 56

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 40 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGTC	GTCAGGTAGG	CGTTCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACCTGGTA	150
	GAGATGGAAAG	TTCTGTAACT	GCTGTCTCAG	TACGATTTC	CAGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAMGCA	250
	AGTGGGAAGM	GAAAATCATC	GARCTGGCTG	GCTTCTGGAA	TTCTTACATC	300
50	CCAGAACCAAG	AGCGTGGCAT	TGACAAGCCA	TTCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTWGAGC	400
	GCGGTATCAT	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
55	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CGAAGCCAGG	CTCAATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAAC TG	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GGCGACAAACAT	CAAGATGGTT	GTGACGCTGA	TCCACCCAAAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 57

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG TGAGCACATC CTGCTGGTC GTCAGGTAGG CGTTCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACCTGGTT GAGATGGAAG TGCGCGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACCCCCATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCAGCGCTG 25 AGTGGGAAGC GAAAATCATC GAGCTGGCAG GTCACCTGGA TTCCTACATC CCGGAAACCGG AGCGTGCAT TGACAAAGCCG TTCTGCTGTC CGATCGAAGA CGTATTCTCC ATCTCYGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT CAAGGTTGGT GAAGAAAGTTG AAATCGTGGG CATCAAAGAC ACCAGCGAAAT CCACCTGTAC CGGCCTTGAA ATGTTCCGCA AACTGCTGGA 30 CGAAGGCCGT GCGGGCGAGA ACGTAGGTT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCCATCAAG CCGCACACCA AGTTCGAACAT TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 35 GTACRACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC GTTTCGCAAT C	50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 831
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40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55	CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATATA CATCGTTGTT TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGGCGACG 60 ATGTTCCCTGT AATCGCTGGT TCTGCTTGA AAGCTCYTGA AGGCGATGCT	50 100 150 200 250
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	TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACTG	300
	TCCAACCCA GAACGTGACA CTGACAAACC ATTCACTGATG CCAGTCGAAG	350
	ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGGTGAAG	400
	CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA	450
5	AGAAAATGCT AAAACAACCTG TAACTGGTGT TGAAATGTTG CGTAAATTGT	500
	TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACAGTGGTGT	550
	GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT	600
	CACACCTCAT ACAAAATTAA AAGCTGAAGT TTACGTTTTA ACAAAAGAAG	650
	AAGGTGGACG TCACACACCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC	700
10	TTCCGTACAA CTGACGTAAC TGGTGTGTT GAATTACCAAG AAGGAACGTGA	750
	AATGGTTATG CCTGGTGATA ACGTAACAAT CGACGTTGAA TTGATCCACC	800
	CAATCGCTAT CGAAGACGGA ACTCGTTCT CAATT	835

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
- (B) STRAIN: ATCC 43198

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT TAGTAGTATC TGCTGCTGAT GGTCTATGC CACAAACTCG	50
	TGAACACATT CTTTATCAC GTAACGTTGG TGTTCCATAC ATCGTTGTT	100
	TCTTAAACAA AGTTGATATG GTTGACGACG AAGAATTATT AGAATTAGTT	150
35	GAAATGGAAG TACGTGACTT ATTAACGTAA TACGACTTCC CAGGAGACGA	200
	TGTTCCCTGTA ATCGCTGGTT CTGCATTAAA AGCTTTAGAA GGCAGACCAT	250
	CTTACGAAGA AAAAATCTTA GAATTAATGG CTGCAGTTGA CGAATACATC	300
	CCAACCTCCAG AACGTGACAA CGATAAACCA TTCATGATGC CAGTCGAAGA	350
	CGTATTTCA ATCACTGGTC GTGGTACTGT TGCTACAGGT CGTGGTGAAC	400
40	GTGGACAAGT ACGTGGTGGT GACGAAGTTG AAATAGTTGG TATCCATGAT	450
	GAAATTTCTA AAACAACAGT TACTGGTGT GAAATGTTCC GTAAATTATT	500
	AGATTACGCT GAAGCTGGAG ACAACATCGG TGCATTATTA CGTGGTGTGG	550
	CTCGTGAAGA TATCCAACGT GGTCAAGTAT TAGCTAAACC AGGTTCAATC	600
	ACTCCACATA CAAAATTCACT TGCTGAAGTG TACGTTTTAA CTAAAGAAGA	650
45	AGGTGGACGT CATACTCCAT TCTTCACTAA CTACCGTCCA CAATTCTACT	700
	TCCGTACAAC TGACGTTACA GGTGTAGTTA ACTTACCAAGA AGGTACTGAA	750
	ATGGTTATGC CTGGTGATAA CGTAACATAG GAAGTTGAAT TAATCCACCC	800
	AATCGCTATC GAAGACGGAA CTCGTT	826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

	CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGCCTATG CCTCAAACTC	50
10	GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTCCTTA CATCGTCGTT	100
	TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG	200
	ACACTCCAGT TATCGCAGGT TCAGCTTGA AAGCCTTAGA AGGCACGCT	250
	TCATATGAAG AAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT	300
	CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCACTGATG CCAGTCGAAG	350
15	ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA	400
	CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA	450
	AGAAAATGCT AAAACTACTG TAACAGGTGT TGAAATGTT CGTAAATTGT	500
	TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG	550
	GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT	600
20	CACTCCACAT ACAAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG	650
	AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC	700
	TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAAG AAGGTACTGA	750
	AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC	800
	CAATCGCGAT CGAAGACGGT ACTCGTTCT CAATC	835

25

2) INFORMATION FOR SEQ ID NO: 61

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 835 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

45	CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCTATG CCTCAAACTC	50
	GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTCCTTA CATCGTYGTA	100
	TTCTTGAACA AAGTAGATAT GGTCGATGAC GAAGAATTAC TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTG CCTGGTGACG	200
	ATGTTCTGT AATCGCTGGT TCAGCTTGA AAGCTTCTAGA AGGCACGCT	250
	TCATACGAAG AAAAATCTT TGAATTAATG GCTGCAGTTG ACGAATATAT	300
50	CCCAACTCCA GAACGTGACA ACGACAAACC ATTCACTGATG CCAGTTGAAG	350
	ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA	400
	CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTT GTATCGCAGA	450
	AGAAAACAGCT CAAACAAACAG TTACTGGTGT TGAAATGTT CGTAAATTAT	500
	TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTACT ACGTGGTGT	550
55	GCACGTGAAG ACATCCAACG TGGACAAGTT TTGCTAACAC CAGGTACAAT	600
	CACKCCTCAT ACAAAATCT CTGCAAGT ATACGTGTT ACTAAAGAAG	650
	AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC	700
	TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAAG AAGGAACGTGA	750
	AATGGTTATG CCTGGCGACA ACGTAACAAAT GGAAAGTTGAA TTAATCCACC	800
60	CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC	835

2) INFORMATION FOR SEQ ID NO: 62

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT	50
	TATTATCACG TAACGTTGGT GTACCATAACA TCGTTGTATT CTTAAACAAA	100
	ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT	150
	TCGTGACTTA TTATCAGAAT ACGATTCCC AGGCGATGAT GTTCCAGTTA	200
	TCGCAGGTTC TGCTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA	250
25	AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA	300
	ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA	350
	TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT	400
	CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA	450
	AACAACTGTT ACAGGGTGTG AAATGTTCCG TAAATTATTA GACTACGCTG	500
30	AAGCAGGCAGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT	550
	ATCGAACGTG GACAAGTTATT AGCTAAACCA GCTACAATCA CTCCACACAC	600
	AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC	650
	ACACTCCATT CTTCACTAAC TACCGTCCCTC	680

35

2) INFORMATION FOR SEQ ID NO: 63

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

55	AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT	50
	TATTATCACG TAACGTTGGT GTACCATAACA TCGTTGTATT CTTAAACAAA	100
	ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT	150
	TCGTGACTTA TTATCAGAAT ACGATTCCC AGGCGATGAT GTTCCAGTTA	200
	TCGCAGGTTC TGCTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA	250
	AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA	300
	ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA	350
60	TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT	400

	CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA	450
	AACAACGTGTT ACAGGTGGTG AAATGTTCCG TAAATTATTA GACTACGCTG	500
	AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT	550
5	ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC	600
	AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGC GGACGTC	650
	ACACTCCATT CTTCACTAAC TACCGTCCTC	680

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25	AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACTCGT GAACACATCC	50
	TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA	100
	GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT	150
	TCGTGACCTA TTAACAGAAT ACGAATTCCC TGTTGACGGAT GTTCCTGTAG	200
30	TTGCTGGATC AGCTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA	250
	AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA	300
	ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA	350
	TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT	400
	CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACCTCAAA	450
35	AACAAACAGTT ACTGGTGTG AAATGTTCCG TAAATTGTTA GACTACGCTG	500
	AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC	550
	ATCCAACGTG GACAAGTTT AGCTAAACCA GGTACAATCA CACCTCATAC	600
	AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC	650
	ATACTCCATT CTTCACTAAC TACCGTCCTC AATTT	685

40

2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavesiens*
- (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

60	CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC	50
	GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT	100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGGCAGC	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTGA	AAGCTCTTGA	AGGCAGATGCT	250
	TCATACGAAG	AAAAAAATCAT	GGAATTAAATG	GCTGCAGTTG	ACGAATAACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCAATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAAATGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
10	TAGACTATGC	TGAAGCAGGG	GATAAACATTG	GTGCATTGCT	ACGTGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAAATTAA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTT	GAATTACCAAG	AAGGAACCTGA	750
15	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGG	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACATCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATAACAT	CGTTGTTTTC	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCA	GGCGACGATG	TTCCGTAAAT	CGCCGGTTCT	GCTTTGAAAG	200
40	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	CGCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACGTAA	CAGGTGTTGA	450
5	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTA	600
	TGTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAAC	TC	50
GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA		100
TTCTTGAACA AAGTAGATAT GGTTGACGAC GAAGAAATTAC TAGAATTAGT		150
10 TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTTC CCTGGTGACG		200
ATGTTCTGT AGTTGCTGGT YCAGCTTGA AAGCTTCTAGA AGGCAGCGCT		250
TCATACGAAG AAAAACCTCT TGAATTGATG GCTGCAGTTG ACGAATATAT		300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCAATGATG CCAGTCGAAG		350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGGTGAAG		400
15 CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA		450
AGAAAACAGCT CAAACAAACAG TTACTGGTGT TGAAATGTT CGTAAATTAT		500
TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACAGTGGTGT		550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT		600
CACACCTCAT ACAAAATTCT CTGCAGAAAGT ATACGTGTTG ACAAAAGAAG		650
20 AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC		700
TTCCGTACRA CTGACGTAAC AGGTGTTGTT GAATTACCAAG AAGGAACGTGA		750
AATGGTTATG CCTGGCGACA ACGTAACAAAT GGAAGTTGAA TTAATCCACC		800
CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC		835

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAAC	TC	50
GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCAATA CATCGTTGTA		100
45 TTCTTGAACA AAGTAGATAT GGTTGATGAC GAAGAAATTAC TTGAATTAGT		150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTTC CCTGGTGACG		200
ATGTTCTGT AATCGCTGGT TCAGCTTAA GAGCTTCTAGA AGGCAGCGCT		250
KCATACGAAG AAAAACCTCT TGAATTGATG GCTGCAGTTG ACGAATATAT		300
CCCAACTCCA GAACGTGATA ACGACAAACC ATTCAATGATG CCAGTTGAGG		350
50 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACAGTGGTGAAG		400
CGTGGACAAG YTCTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA		450
AGAAAACAGCT CAAACAACTG TAATCTGGTGT TGAAATGTT CGTAAATTAT		500
TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACAGTGGTGT		550
TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT		600
55 CACACCTCAT ACAAAATTCT CTGCAGAAAGT ATACGTGTTG ACTAAAGAAG		650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC		700
TTCYGTACGA CTGACGTAAC TRGTGTTGTY GAATTACCAAG AAGGAACGTGA		750
AATGGTTATG CCTGGCGACA ACGTAACAAAT GGAAGTTGAA TTAATCCACC		800
CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC		835

60

2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
- (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

20	CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACAC	50
	GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCCTTA CATCGYTGTA	100
	TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGATTTCCAGCGACG	200
	ACACTCYAGT TATCGCTGGT TCAGCYTTGA AAGCTTTAGA AGGCGACCCT	250
25	TCATACRAAG AAAAATCTT AGAATTAAATG SCTGCTGTTG AGGAATACAT	300
	CCCAACACCA GTTCGTGATA CTGACAAACC ATTCAATGATG CCAGTCGAAG	350
	ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA	400
	CGTGGACAAG TTTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA	450
	AGAAAATGCT AAAACAACGT TTACAGGTGT TGAAATGTT CGTAAATTGT	500
30	TAGACTACGC TGAAGCAGGC GATAAACATCG GTGCATTATT ACGTGGTGT	550
	GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAC CAGCTTCAAT	600
	CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG	650
	AAGGGGGCG TCACACTCCG TTCTTCACTA ACTACCGTCC TCAGTTCTAC	700
	TTCCGTACAA CTGACGTAAC TGGTGTGTT GATCTACCAAG AAGGTACTGA	750
35	AATGGTAATG CCTGGTGATA ACGTAACAT GGAAGTTGAA TTAATCCACC	800
	CAATCGCGAT CGAAGACGGA ACTCGTTCT CTATTC	836

2) INFORMATION FOR SEQ ID NO: 70

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
- (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACTC	50
	GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCCTTA CATCGTTGTA	100
	TTCTTAAACA AAATGGATAT GGTTGACGAT GAAGAATTAC TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTAACGTGATACGACTTC CCAGGGCGACG	200
	ACACTCCAGT TATCGCAGGT TCAGCTTGA AAGCCTTAGA AGGCGACGCT	250
60	TCATACGAAG AAAAATCTT AGAATTAAATG GCTGCTGTTG ATGAATACAT	300

	CCCAAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGYGGAAAG	350
	ACGTAYTCTC	AATCACTGGT	CGTGGAACTG	TGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATTGCTGA	450
5	AGAAAATGCT	AAAACAACGT	TTACAGGTGT	TGAAATGTT	CGTAAATTGT	500
	TGGATTACGC	TGAAGCGGGC	GACAACATTG	GTCATTATT	ACGTGGTGT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCCGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTAGTT	GATCTACCA	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACATAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCGAT	CGAAGACGGA	ACTCGTTCT	CTATT		835

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- 20 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
- (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

30	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACTC	50
	GTGAACACAT	CTTGTATCT	CGTAACGTAG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTC	CCAGGCGATG	200
35	ACACTCCAGT	TATTGCAAGT	TCTGCTTGA	AAGCTTTAGA	AGGCGATCCA	250
	GTTCACGAAG	AAAAAAATCTT	CGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGAAAAACC	ATTATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
40	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GAAATCGTTG	GTATCGACGA	450
	AGAAAACAGCT	CAAACACTG	TAACAGGTGT	TGAAATGTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCTTTATT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAC	CAGGAACAAT	600
	CACTCCTCAT	ACAAAATTG	TAGCTGAAGT	TTACGTTTTA	ACTAAAGAAG	650
45	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTA	GAATTACGCG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTAACATAT	CGACGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTCT	CTATT		835

50

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- 55 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGTT	ATTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCCG	TAACATTGGT	ACTTTGTTAC	GTGGTGTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
20	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTGAC	TAAAGAAGAA	650
	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGGCATAT	TTTGCTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAAT	TGCTGACTGA	ATATGATTT	CCTGGCGACG	200
	ACATT CCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	AAAAAGTCGG	GGATGAAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTC	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
55	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTTGTT	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTGTTACCA	AAGGAACGGA	750
	AATGGTGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

60

2) INFORMATION FOR SEQ ID NO: 74

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: ATCC 15305

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCAAT	GATTATAAAC	50
AATCAATATA	CGATTGGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
AGATTCTGGT	TTTTAAATT	CAAAAAGTTT	TCTAAAAAAAT	TTACTTGCTT	200
TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	AAAACAGTA	AAGGAAATGA	250
ATCATGAAAC	AATTAACCAA	GCCTTATAC	TTTACCTAT	TACTTTTAT	300
25 TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTGGTG	GACGCCCGTT		380

30 2) INFORMATION FOR SEQ ID NO: 75

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 49996

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
GCATATTGGT	CTTTCTCGTC	AAAGGGGTGT	GAAACATTG	ATCGTCTTTT	100
TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTTAGTTGAA	150
ATGGAAGTCA	GAGAATTGCT	GACTGAATAT	GATTTCCCTG	GCGACGACAT	200
55 TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAAGGG	GACCCAGATG	250
CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCC	300
ACGCCAGAAC	GTGATACTGA	CAAACCATTG	TTGTTACCGA	TCGAAGATGT	350
CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCGG	ATCGATCGCG	400
GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCGGAAT	CAAACCTGAA	450
55 ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
GTGATGAAAT	TGAACGTGGC	CAAGTGTAG	CAAACCCAGG	TTCTATCACA	600
CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
CGGTGCCAT	ACCCCCA				666

2) INFORMATION FOR SEQ ID NO: 76

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

20	TGGTGCATT TTAGTTGTAT CCGAACAGA TGGTCCAATG CCTCAAACCC	50
	GGGAACATAT CTTGCTTCG AGACAAGTT GTGTGAAACA TCTGATTGTT	100
	TTCTTGAACA AAATCGATT AGTCGATGAC GAAGAATTGA TTGATTTAGT	150
	AGAAATGGAA GTAAGAGAAC TGCTATCTGA ATATAATTTC CCAGGGGATG	200
	ACATTCCTGT TATCAAAGGT TCGGCATTAA AAGCGTTGGA AGGAGACCT	250
	GATGCCAGAG CTGCCATCAT GGAATTAAATG GATACAGTAG ACAGCTATAT	300
25	CCCAACACCT GAGCGTGATA CAGACAAAACC ATTACTCTTG CCAGTTGAAG	350
	ATGTCTTTTC GATTACTGGA CGAGGAACAG TTGCTTCGG ACGGATCGAT	400
	CGGGGAACAG TTCGGGTAGG CGATGAAGTA GAAATCGTCG GTATCAAACC	450
	TGAAACCCAA AAAGCTGTAG TGACAGGCGT CGAAATGTTC CGCAAGACGA	500
	TGGACTTTGG GGAAGCCGGT GACAATGTAG GTGCTTGCT GAGAGGGATC	550
30	ACTCGTGACG AAATTGAACG AGGACAAGTG TTGGCTAAAC CAGGTTCGAT	600
	CACACCACAT ACAAAATTCC AAGCAGAAGT TTATGTATTG ACGAAAGAAG	650
	AAGGTGGTCG TCATACACCA TTCTTCAACA ACTATCGTCC ACAATTAT	700
	TTCCGTACAA CGGATGTGAC AGGGAACATT ACATTGCCTG AAGGAACAGA	750
	A	751

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2) INFORMATION FOR SEQ ID NO: 77

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia canis*
- (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

55	TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA	50
	GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG	100
	TGGATGAATA AGTGTGATGT TGTAGATGAT GAAGAAATGT TGTCTATTAGT	150
	TGAAATGGAA ATAAGGGAAT TGTTATCAAAT ATATGGGTAT CCTGGGGATG	200
	ATATAGATGT AGTTAGAGGA TCTGCAGTTA AACGATTAGA AGAAGAAACA	250
	GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA	300
60	AAAAATAAGT TTACCAAGTAA GAGAAAAAGA TAAGCCATT TTAATGTCAA	350

	TAGAAGATGT	GTTCCTTCAATA	CCTGGAAAGAG	GTACAGTAGT	AACAGGAAAGA	400
	ATAGAAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GC GTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTAAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAACCGAGA	GGTATATATA	TTGAAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTCT	CAAATTACCA	GCCGCAATT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

2) INFORMATION FOR SEQ ID NO: 78

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACCTGGT	150
	TGAAATGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGGCAGC	200
	ACACTCCGAT	CGTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCAGACGCA	250
35	GAGTGGGAAG	CGAAAATCCT	GGAACTGGCT	GGCTTCCCTGG	ATTCTTAYAT	300
	TCCGGAAACCA	GAGCGTGCAG	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAACGCCG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGT	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
5	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

5	CGATCCTGGT	AGTTGCTGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
	CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTCCCT	100
	GAACAAGTGC	GACATGGTTG	ATGACGAAGA	GCTGCTGGAA	CTGGTTGAAA	150
	TGGAAGTTCG	TGAACCTCTG	TCTCAGTACG	ACTTCCCAGG	CGACGACACT	200
10	CCGATCGTTC	GTGGTTCTGC	TCTGAAAGCG	CTGGAAGGCG	ACGCAGAGTG	250
	GGAAAGCGAAA	ATCCTGGAAC	TGGCTGGCTT	CCTGGATTCT	TACATTCCGG	300
	AACCAGAGCG	TGCGATTGAC	AAGCCGTTCC	TGCTGCCGAT	CGAAGACGTG	350
	TTCTCCATCT	CCGGTCGTGG	TACCGTTGTT	ACCGGTCGTG	TAGAACGCGG	400
	TATCATCAAA	GTTGGTGAAG	AAAGTTGAAAT	CGTTGGTATC	AAAGAGACTC	450
15	AGAAAGTCTAC	CTGTACTGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
	GGCCGTGCTG	GTGAGAACGT	AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	550
	AGAAATCGAA	CGTGGTCAGG	TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	600
	ACACCAAGTT	CGAATCTGAA	GTGTACATT	TGTCCAAAGA	TGAAGGCAGG	650
	CGTCATACTC	CGTTCTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
20	TACTGACGTG	ACTGGTACCA	TCGAACTGCC	GGAAGGCAGT	GAGATGGTAA	750
	TGCCGGCGA	CAACATCAAA	ATGGTTGTTA	CCCTGATCCA	CCCGATCGCG	800
	ATGGACGACG	GTCTCGTTC	CGCAA			825

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2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia hermannii*
- (B) STRAIN: ATCC 33650

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

45	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCCCGAG	TACGATTTC	CGGGCGACGA	200
	CACCCCGATC	GTTCGTGGTT	CCCGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGA	GAAAATCATC	GAACCTGGCTG	GCTACCTGGA	TTCCCTATATC	300
	CCGGAACCGAG	AGCGTGCAGT	TGACAAGCCG	TTCCTGCTGC	CTATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGT	CGTGTAGAGC	400
50	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTTG	AAATCGTGGG	TATCAAAGAT	450
	ACTCGAAAT	CAACCTGTAC	CGGCCTTGAA	ATGTTCCGCA	AACTGCTGG	500
	CGAAGGCCGT	GCGGGGCAGA	ACGTGGGTGT	TCTGCTGCCT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAACGCCGG	TTCCATCAAG	600
	CCKCACACCA	AGTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
55	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCCGCAG	TTCTACTTCC	700
	GTACAACATGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAAGG	CGTTGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAATGGTT	GTACCCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTCGCAA			829

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GGCTCCGTA	CATCATCGTG	100
20 TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
TGAGATGGAA	GTGCGTGAAC	TTCTGTCCC	GTACGACTTC	CCGGGCGACG	200
ACACCCCGAT	CATTGCGTGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCAGAAGCT	250
GAGTGGGAAG	AGAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCCTACAT	300
CCCGGAACCA	GAGCGTGCAG	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
25 ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
CGCGGTATCA	TCAARGTKGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
TACTGCGAAA	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGTGCG	TGCAGGGCGAG	AACTGCGGCG	TTCTGCTGCG	TGGTATCAAG	550
CGTGAAGAGA	TCCAGCGTGG	CCAGGTTCTG	GCTAAGCCGG	GCTCAATCAA	600
30 GCCGCACACC	AAGTTCGAAT	CCGAAGTGT	CATCCTGTCC	AAAGACGAAG	650
GCGGCCGTCA	CACTCCGTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
CGTACAAC	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAAACA	TCAAAATGGT	TGTTACCTG	ATCCATCCGA	800
TCGCGATGGA	CGACGG				816

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2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lenthum*
 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCCTCC	TCGTTATCGC	CGCCACCGAC	GGCCCGATGG	CCCAAGACCCG	50
55 CGAGCACATC	CTGCTCGCCC	GTCAGGTCGG	CGTGCCTAC	ATCGTGGTCT	100
TCCTGAACAA	GTGCGACATG	GTGCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
GAGATGGAAG	TTCGCGAGCT	GCTCGACTCT	TACGAGTTCC	CGGGCGACGA	200
CACCCCGATC	ATCCGCGGCT	CCGCTTTGAA	GGCCCTCGAG	GGCGACAAAG	250
AGTGGCAGGA	GAAGGCTCTGG	GAGCTCATGG	ACGCCGTGCA	CTCCTACATC	300
60 CCGACGCCGG	AGCGCATGGT	CGACAAAGCCG	TTCTGATGG	CCGTCGAGGA	350

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAAC	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
5	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCAG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCACC	TTCCCGAGGG	CACCGAGATG	750
10	GTCATGCCGG	GCGACAAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATT	TGGTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
35	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
	GAGAATGGGC	AGACAAGATT	GTAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCCCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCCCTGA	TGCCTGTAGA	350
	GGACGTATT	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTG	400
40	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
45	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

5	GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA	50
	GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA	100
	TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA	150
	ATGGAAGTTC GYGAACCTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT	200
10	CCCAGTTGTT AAAGGTTCA GCGTCAAAGC ACTGGAAGGC GAAGCAGAGT	250
	GGGAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCA	300
	GAACCAGAGC GTGCGATTGA CAAGCCATTG CTGCTGCCAA TCGAAGACGT	350
	ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG	400
	GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT	450
15	GTAAAGTCTA CTTGTAATGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA	500
	AGGCCGTGCY GGTGAGAACG TTGGTTTCT GCTGCGTGGT ATCAAGCGTG	550
	AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAAGGTT AATCAAACCA	600
	CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCAG	650
	CCGTCATACT CCGTTCTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA	700
20	CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCAGT AGAGATGGTA	750
	ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC	800
	GATGGATGAC GGTCTGCGTT TCGCAA	826

25 2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 35 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Francisella tularensis*
 - (B) STRAIN: LVS

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

45	TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC	50
	GTGAGCACAT TCTGCTTCT CGTCAAGTTG GTGTACCAAA AATCGTTGTT	100
	TTCTTAAACA AGTGTGACAT GGTTGATGAT GAAGAGTTAT TAGAGCTAGT	150
	TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG	200
	ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA	250
	GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT	300
	TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTATTCTT CCGATCGAAG	350
	ATGTATTCTC AATTTCAGGT CGTGGTACTG TTGTAACCTGG TCGTATTGAG	400
50	CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTGTC	450
	AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTAG	500
	ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCTTAGTTG TGGACTTAAG	550
	AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAAGCCAG GTCAATTAA	600
	GCCACATACT AAGTTTGAAG CTGAGGTTTA TGATTATCT AAAGAAGAGG	650
55	GTGGTAGACA TACTCCATTG TTCAAGGGAT ATAGACCACA ATTCTACTTC	700
	CGTACTACAG ACATTACTGG AGCTGTTGAG CTCCAGAGG GTGTAGAAAT	750
	GGTTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA	800
	TCGCTAGGAT GAAGGGTTAC GTTTTGCA	828

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

CGGTGCTATC	ATCGTAGKTG	CTGCTACTGA	TGGTCCGATG	CCTCARACTC	50
GTGAGCAYAT	CYTGCTGGCT	CGTCAGGTAA	ACGTWCCKAG	ACTGGTTGTA	100
20 TTCATGAACA	AGTGYGACAT	GGTAGACGAC	GCTGAAATGY	TGGAACTCGT	150
TGAAATGGAA	ATGCGTGAAC	TGCTTTCAGC	YTACGAATTG	GAYGGYGACA	200
ACACTCCKTT	CATTCAAGGGT	TCTGCTCTTG	GTGCRTTGAA	YGGCGTTGAA	250
AAGTGGGAAG	AGAAGGTTAT	GGANCTGATG	GATGCTTGCG	ACACTTGGAT	300
25 TCCTTTGCCT	CCGCGTGATA	TTGAYAAACC	GTTCTTGATG	CCGGTTGAAG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCTACTGG	TCGTATCGAA	400
GCTGGTGTAA	TCCATGTAGG	TGACGAAGTT	GAAATCCTCG	GTTTGGGTGA	450
AGACAAGAAG	TCTGTTGTA	CTGGTGTGA	AATGTTCCGC	AAGTTGCTGG	500
20 ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTY	TGTTGCTCCG	TGGTATCGAC	550
AAGAACGAAA	TCAAACGTGG	TATGGTTCTT	TGTAAGCCCC	GTCAGATTAA	600
30 ACCTCACTCT	AAGTTCAAAG	CTTCTATCTA	CGTTTGAAAG	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCGTTC	CACAACAAAT	ACCGTCCTCA	GTTCTATCTG	700
CGTACTATGG	ACTGTACAGG	TGAAATCWCT	CTTCCGGAAG	GAACTGAAAT	750
GGTAATGCCT	GGTGATAACG	TAGAAATCAC	TGTAGAACTG	ATCTACCCGG	800
35 TAGCATTGAA	CGTAGGTTG	CGTTTCGCT			829

35

2) INFORMATION FOR SEQ ID NO: 87

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

CTATCTTAGT	AATCGCTGCT	ACAGATGGAC	CAATGGCTCA	AACTCGTGAG	50
55 CACATCCTAT	TATCTCGTAA	CGTTGGAGTA	CCAAAAATCG	TTGTATTCTT	100
AAACAAATGT	GATATGGTTG	ATGACGAAGA	GTTATTAGAA	TTAGTTGAAA	150
TGGAAAGTTCG	TGAACATTAA	TCTGAATACG	GATTGACGG	AGATGAACTA	200
CCAGTAATCA	AAGGTTCTGC	TCTTAAAGCT	CTTGAAGGAG	ATGCAGATGC	250
AGAAAAAAGCT	ATCATCGAAT	TAATGGAAAC	AGTTGACGAA	TACATCCCAA	300
60 CTCCAGAACG	TGATAACGCT	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350

	TTCTCAATCA	CAGGTCGTGG	TACAGTTGCT	ACTGGACGTG	TTGAACGTGG	400
	ACAAGTTAAA	GTTGGAGACG	TAGTAGAAAT	CGTTGGATTA	ACTGAAGAAC	450
	CAGCTTCAAC	TACTGTAACA	GGTGTGAAA	TGTTCCGTAA	ATTATTAGAT	500
5	TACGCTGAAG	CAGGAGATAA	CATCGGTGCA	TTATTACGTG	GTGTTGCTCG	550
	TGAAGACATC	GAACGTGGAC	AAGTTTAGC	AGCTCCTAAA	ACAATCACTC	600
	CACACACTCA	ATTCTGTAGCT	GACGTGTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CACAAACTAC	CGTCCTCAAT	TCTACTTCCG	700
	TACTACTGAC	GTAACTGGTG	TAGTTACTTT	ACCAGAAGGT	ACTGAAATGG	750
10	TAATGCCTGG	GGATAACGTA	TCAATCAACG	TAGAACTTAT	TTCTCCAATC	800
	GCGATCGAAG	AAGGAACCTCG	TTTCTCAA			828

2) INFORMATION FOR SEQ ID NO: 88

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Gemella morbillorum*
(B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30	TCTTAGTAAT	CGCTGCTACA	GATGGTCCTA	TGGCTCAAAC	TCGTGAACAC	50
	ATCCTATTAT	CTCGTAACGT	TGGAGTACCT	AAAATTGTTG	TATTCTTAAA	100
	CAAATGTGAT	ATGGTTGATG	ACGAAGAGTT	ATTAGAATTA	GTAGAAATGG	150
	AAGTTCTGTA	ACTATTATCT	GAATACGGAT	TTGATGGAGA	TGAACTACCA	200
	GTAATCAAAG	GTTCAGCTCT	TAAAGCTCTT	GAAGGAGATG	CAGATGCTGA	250
35	AAAAGCTATC	ATCGAATTAA	TGGAAACAGT	TGACGAGTAC	ATCCCACACTC	300
	CAGAACGTGA	TAACGCTAAA	CCATTATGA	TGCCAGTTGA	GGACGTGTTTC	350
	TCAATCACAG	GTCGTGGTAC	AGTTGCTACT	GGACGTGTTG	AACGTGGACA	400
	AGTTAAAGTT	GGTGACGTAG	TAGAAATCGT	TGGATTAACT	GAAGAACCCAG	450
	CTTCAACTAC	TGTAACAGGT	GTTGAAATGT	TCCGTAATT	ATTAGATTAC	500
40	GCTGAAGCAG	GAGATAACAT	CGGTGCATTA	TTACGTGGTG	TTGCTCGTGA	550
	AGATATCGAA	CGTGGACAAG	TTTGTAGCAGC	TCCTAAAACA	ATCACTCCAC	600
	ATACTCAATT	CGTAGCTGAT	GTGTACGTAT	TATCTAAAGA	AGAAGGTGGA	650
	CGTCACACTC	CATTCTTCAC	AAACTACCGT	CCACAATTCT	ACTCCGTAC	700
	TACTGACGTA	ACTGGGTGAG	TTACTTTACC	AGAAGGTACT	GAAATGGTAA	750
45	TGCCTGGGGA	CAACGTATCA	ATCAACGTAG	AACTTATTTC	TCCAATCGCT	800
	ATCGAAGAAG	GAACTCGTTT	CTC			823

50 2) INFORMATION FOR SEQ ID NO: 89

 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

5	GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA	50
	GCACATCTTA TTAGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT	100
	TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA	150
	ATGGAAGTTC GTGAACCTCT TTCTCAATAT GACTTCCCAG GCGATGACAC	200
10	CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAGGC GATGCCGCAT	250
	GGGAAGAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG	300
	GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCA TTGAAGATGT	350
	GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG	400
	GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT	450
15	GCAAAACCA CCGTAACCGG TGTTGAAATG TTCCGTAAT TACTTGACGA	500
	AGGTCGTGCG GGTAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG	550
	AAGAAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG	600
	CACACTGACT TCGAATCTGA AGTGTACGTA TTGTCAAAG AAGAAGGTGG	650
	TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATT TATTTCGTA	700
20	CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT	750
	ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC	800
	GATGGACCAA GGTACGTT TCGCTATCG	829

25 2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus aphrophilus*
- (B) STRAIN: ATCC 33389

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

45	TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC	50
	GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTCCTTA CATCATCGTA	100
	TTCTTAAACA AATGCGACAT GGTAGATGAC GAAAGAGTTAT TAGAATTAGT	150
	TGAAATGGAA GTTCTGAAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG	200
	ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCCTTGCA	250
	GAATGGGAAG AAAAATCCT TGAATTAGCA AACCACTTAG ATACTTACAT	300
	TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCTTCTT CCAATTGAAG	350
	ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGGTGAG	400
50	CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC	450
	GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG	500
	ACGAAGGTGCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA	550
	CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC	600
	TCCGCACACT GATTCGAAT CTGAAGTGTG CGTATTATCC AAAGAAGAAG	650
55	GTGGTCTCA TACTCCATTG TTCAAAGGTT ACCGTCCACA ATTCTATTTC	700
	CGTACAACGTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAAT	750
	GGTTATGCCG GGCATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA	800
	TCGCGATGGA CCAAGGTTA CGTTTCGCTA TCG	833

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

CGGCCTATC	TTAGTTGTAG	CAGCAACTGA	TGGTCCTATG	CCTCAAAC	TC	50
GTGAAACACAT	CTTATTAGGC	CGCCAAGTTG	GTGTTCCCTTA	CATCATCGTA		100
20 TTCTTAAATA	AATGCGATAT	GGTAGATGAT	GAAGAATTAT	TAGAATTAGT		150
TGAAATGGAA	GTTCTGTGAA	TTCTTCTCA	ATATGATTTC	CCAGGTGACG		200
ATACTCCTAT	CGTTCTGGT	TCAGCATTAC	AAGCATTAAA	TGGTGTGCCT		250
GAGTGGGAAG	AAAAAAATCAT	TGAATTAGCA	CAACACTTAG	ATTCTTATAT		300
CCCTGAGCCT	GAGCGTGC	TTGATAAAC	TTTCTTATTA	CCAATCGAAG		350
25 ACGTATTCTC	AATTCAGGT	CGTGGTACAG	TAGTAACC	TCGTGTTGAG		400
CGTGGTATCA	TCAAATCAGG	TGAAGAAGTT	GAAATCGTAG	GGATTAAAGA		450
AACGACAAAA	ACAACAGTAA	CCGGTGTGAA	GATGTTCCGT	AAACTATTAG		500
ACGAAGGTG	TGCGGGTGAA	AACGTAGGTG	CCTTATTACG	TGGTACTAAA		550
CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTACAATTAC		600
30 ACACACACT	GATTTGAAT	CAGAAGTTA	TGTATTATCA	AAAGAAGAAG		650
GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ATCGTCCTCA	GTTCTACTTC		700
CGYACAACGG	ACGTAACAGG	AACGATTGAA	TTACCTGAAG	ATGTTGAGAT		750
GGTAATGCCT	GGTGATAATA	TCAAGATGAC	AGTAAGCTT	ATTCAACCTA		800
TCGCGATGGA	CGAAG					815

35

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

TGGTGCATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCAATG	CCACAAAC	TC	50
55 GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCCATA	CATCATCGTA		100
TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT		150
AGAAATGGAA	GTTCTGTGAA	TTCTTCTCA	ATATGACTTC	CCAGGTGACG		200
ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCATTAAA	TGGCGTAGCA		250
GAATGGGAAG	AAAAAAATCT	TGAGTTAGCA	AACCCTTAG	ATACTTACAT		300
60 CCCAGAACCA	GAGCGTGC	TTGACCAACC	GTTCCTTCTT	CCAATCGAAG		350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGA	AATGTTCCGT	AAATTACTTG	500
5	ACGAAGGTGCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGTT	ACCGTCCACA	ATTCTATTTC	700
	CGTACAAC TG	ACGTAAC TGG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
10	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
	TCGCGATGGA	CCAAGGTTA	CGTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 93

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Haemophilus parahaemolyticus*
(B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATT	GTTGAAATGG	150
	AAGTGC GTGA	ACTTCTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTCA CGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGGGA	250
35	AGAAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATT	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAA	GACACTGCGA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGC GGGTGC	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAAGTG	TACGTATTAT	CAAAAGAAGA	AGGTGGTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTA ACT	GGTACTATTG	AATTACCGA	AGGC GTAGAA	ATGGTAATGC	750
45	CAGGC GATAA	CATCAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTG	GATT			824

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

5	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCTTA	CATCATCGT	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTCTCA	ATATGACTTC	CCGGGTGACG	200
10	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCGTTAAA	CGCGTGWCA	250
	GAATGGGAAG	AAAAAATCCT	TGAATTAGCT	AGCCACTTAG	ATTCTTACAT	300
	TCCTGAGCCT	CAACGTGCTA	TCGACCAACC	GTTCTTCTT	CCAATCGAAG	350
	ACGTGTTCTC	TATCTCCGGT	CGTGGTACAG	TAGTAACAGG	TCGTGTTGAG	400
	CGTGGTATCA	TCCGTACCGG	TGATGAAGTT	GAAATCGTAG	GTATCAAACC	450
15	GACTGCGAAA	ACTACCGTAA	CCGGTGTGAA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTGCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACYAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTG	GCTAAACCAG	GTTCAATCAC	600
	TCCACACACT	GATTTCGAAT	CTGAAGTGTAA	CGTATTATCC	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTG	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTC	700
20	CGTACAACGT	ACGTAACCGG	AACTATCGAA	TTACCGGAAG	GCGTGGAAAT	750
	GGTTATGCCT	GGTGATAACA	TCAAAATGAC	TGTATCCTTA	ATCCACCCAA	800
	TCGCGATGGA	CCAAGGTTA	CGTTTCGCTA	TCG		833

25

2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus paraphrophilus*
- (B) STRAIN: ATCC 29241

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

45	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCTTA	CATCATCGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTCTCA	ATATGACTTC	CCGGGTGACG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCGTTAAA	CGCGTGWCA	250
	GAATGGGAAG	AAAAAATCCT	TGAATTAGCA	AACCACTTGG	ATACTTACAT	300
	TCCTGAGCCA	CAACGTGCTA	TCGACCAACC	GTTCTTCTT	CCAATCGAAG	350
	ACGTGTTCTC	TATCTCCGGT	CGTGGTACAG	TAGTAACAGG	TCGTGTTGAG	400
50	CGTGGTATCA	TCCGTACCGG	TGATGAAGTT	GAAATCGTAG	GTATCAAACC	450
	GACTGCGAAA	ACTACCGTAA	CCGGTGTGAA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTGCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTG	GCTAAACCAG	GTTCAATCAC	600
	TCCACACACT	GATTTCGAAT	CTGAAGTGTAA	CGTATTATCC	AAAGAAGAAG	650
55	GTGGTCGTCA	TACTCCATTG	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTC	700
	CGTACAACGT	ACGTAACCGG	TACTATCGAG	TTACCGGAAG	GCGTGGAAAT	750
	GGTAATGCCT	GGCGATAACA	TCAAAATGAC	CGTATCCTTA	ATCCACCCAA	800
	TCGCGATGGA	CCAAGGTTA	CGTT			824

60

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

	GCTATCTTAG	TAGTAGCAGC	AACGTGTTG	CCTATGCCAC	AAACTCGTGA	50
	GCACATCTTA	TTAGGTCGCC	AAGTAGGTGT	TCCTTACATC	ATCGTATTCT	100
20	TAAACAAATG	CGACATGGTA	GATGACGAAG	AGTTATTAGA	ATTAGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	TTCTCAATAT	GACTTCCAG	GTGATGATAAC	200
	TCCAATCATT	CGTGGTTCTG	CATTACAAGC	GTAAACGGC	GTAGCAGAAT	250
	GGGAAGAAAA	AATCCTTGAA	TTAGCTCAAG	CATTAGATAC	TTACATTCT	300
	GAACCTGAGC	GTGCAATCGA	CCAACCGTTC	CTTCTTCAA	TTGAAGACGT	350
25	GTTCTCAATC	TCTGGTCGTG	GTACTGTAGT	AACAGGTCGT	GTAGAGCGTG	400
	GTATCATCCG	TACCGGTGAT	GAAGTTGAAA	TCGTTGGTAT	CAAACCAACT	450
	GCGAAAACAA	CCGTAACCGG	TGTTGAAATG	TTCCGTAAAT	TACTTGACGA	500
	AGGTCTGCA	GGTAAAACA	TCGGTGCATT	ATTACGTGGT	ACTAAACGTG	550
	AAGAAATCGA	ACGTGGTCAA	GTATTAGCGA	AACC GGTT	AATCACTCCA	600
30	CACACTGACT	TCGAATCTGA	AGTGTACGTA	TTATCTAAAG	AAGAAGGTGG	650
	TCGTCTACT	CCATTCTTCA	AAGGTTACCG	TCCACAATTC	TATTTCCGTA	700
	CAACTGACGT	AACCGGTACT	ATCGAGTTAC	CGGAAGGCGT	GGAAATGGTT	750
	ATGCCTGGCG	ATAACATCAA	AATGACCGTA	TCCTTAATCC	ACCCAATCGC	800
	GATGGACCAA	GGTTTACG				818

35

2) INFORMATION FOR SEQ ID NO: 97

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

	CGCGCGTATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	CGCTTCCTTW	CATCATCGTR	100
55	TTCCTGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAACCTGGT	150
	AGAAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCWGGYATG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGYGMACCT	250
	GAGTGGGAAG	CTAACGATCGT	AGAACTGGCT	GAAAATCTGG	ATTCTTACAT	300
60	YCCACARCCA	GAACGTGCTA	TCGAYAAGCC	ATTCCTGCTG	CCAATCGAAG	350

	ACGTATTCTC	TATCTCTGGC	CGTGGTACWG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GARATCGTTG	GTATCAAAGA	450
	TACCGTTAAA	TCAACTTGTA	CCGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
5	ACGAAGGTCG	TGCAGGCGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGACA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GYTCYATCAA	600
	GCCACACACC	AAGTTCGAAT	CAGAAGTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGYCGTCA	TACTCCGTTTC	TTCAAAGGCT	ACCGTCCACA	GTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	TTGCCAGAAG	GCGTGGAAAT	750
	GGTAATGCCA	GGC				763

10

2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
- (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

30	CGGCGCAATC	TTGGTATGTT	CAGCAGCTGA	CGGT CCTATG	CCACAAACTC	50
	GCGAACACAT	CTTGTGGCT	CGCCAAGTAG	GTGTACCTTA	TATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTCGATGAT	GCTGAGTTGT	TGGAATTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGTTGTCTAG	CTACGATTTT	CCAGGCGACG	200
	ATTGCCAAT	CGTTCAAGGT	TCTGCATTGC	GYGCATTGGA	AGGCGACGCT	250
35	GCATACAAAG	AAAAAATCTT	TGAATTGGCT	GCTGCTTGG	ATAGCTACAT	300
	TCCTACTCCA	GAACGTGCTG	TTGATAAAC	ATTCTTGGT	CCAATCGAAG	350
	ATGTATTCTC	TATCTCTGGT	CGTGGTACAG	TAGTTACTGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTAGG	CGAAGAGATT	GAAATCGTTG	GTTTGAAAGA	450
	CACGCAAAAA	ACCACTTGTA	CTGGCGTGG	AATGTTCCGC	AAATTGTTGG	500
40	ACGAAGGTCA	AGCTGGTGAT	AACGTTGGTG	TATTATTGCG	TGGTACGAAG	550
	CGTGAAGACG	TTGAACGTGG	TCAGGTATTG	GCTAAACCAG	GTTCTATCAC	600
	TCCGCACACT	AAATTGAAAG	CTGAAGTGT	TGTGTTGAGC	AAAGAAGAAG	650
	GTGGCCGTCA	TACGCCATTC	TTCGCTAACT	ACCGCCCACA	ATTC TACTTC	700
	CGTACGACTG	ACGTAACCTGG	TGCAGTTACT	TTGTCTGAGG	GTGTGGAAAT	750
45	GGTTATGCCA	GGCGAAAACG	TGAAAATCAC	TGTTGAGTTG	ATTGCACCTA	800
	TCGCTAGGAA	AACGGTTGCG	GTTTGCGC			828

2) INFORMATION FOR SEQ ID NO: 99

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGTC	GTCAGGTAGG	CGTTCCTGAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCCACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCGTGGTT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAATCATC	GAACCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCCT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAACGCCGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAAC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCA	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTCGCA			828

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTCCTG	AACAAGTGC	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAAGTTCGT	GAACCTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTCG	TGTTCTGCT	CTGAAAGCGC	200
45	TGGAAGGCAG	CGCWGAGTGG	GAAKCKAAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCCGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTCC	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGTCGTTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATTY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTACTGGCG	TTGAAATGTT	450
50	CCGAAACTG	CTGGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCCTCAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCG	700
55	GAAGGCGTAG	AGATGGTTAT	GCCGGCGAC	AAACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

60

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

15	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	TGAAATGGAA	GTTCGTGAGC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTCCTGTT	TCCGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
20	GACTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCAG	TTGACAAGCC	GTTCCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGCTAAR	TCWACCTGTA	CYGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
25	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCTCTATCAA	600
	GCCGCACACC	AAGTCGAAT	CTGAAGTGTG	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
30	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCCTG	ATTCAACCR	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

50	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCCTGAAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAACTGG	TTGAGATGGA	150
	AGTTCTGAA	CTGCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACCCCCGA	200
55	TCGTTCTGTT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAACCTGGC	TGGCCACCTG	GATACTATA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTAG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AAACCGCGAA	450
60	AACCACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAC TGCTG	GACGAAGGCC	500

	G TGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAACGCCG	GGCACCATCA	ACCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATCCTGTC	CAAAGACGAA	GGCGGCCGTC	650
5	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGCGACAAAC	ATCAAAATGG	TTGTTACCCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

	GCAGACTCGT	GAGCACATCC	TGCTGGTCTG	TCAGGTAGGC	GTTCGTACA	50
	TCATCGTGT	CCTGAACAAA	TGCGACATGG	TTGATGACGA	AGAGCTGCTG	100
	GAACGGTTG	AGATGGAAGT	TCGTGAACTG	CTGTCTCAGT	ACGATTCCC	150
30	GGCGGACGAC	ACTCCGATCG	TTCGTGGTTC	TGCTCTGAAA	GCGCTGGAAG	200
	GCGACGCAGA	GTGGGAAGCG	AAAATCATCG	AACTGGCTGG	CCACCTGGAT	250
	ACCTATATCC	CGGAACCCAGA	GCGTGCGATT	GACAAGCCGT	TCTGCTGCC	300
	GATCGAAGAC	GTATTCTCCA	TCTCCGGTCG	TGGTACCGTT	GTACCGGTC	350
	GTGTAGAGCG	CGGTATCATC	AAAGTAGGTG	AAGAAGTTGA	AATCGTTGGT	400
35	ATCAAAGAAA	CCCGGAAAAC	CACCTGTACT	GGCGTTGAAA	TGTTCCGCAA	450
	ACTGCTGGAC	GAAGGCCGTG	CTGGTGAGAA	CGTAGGTGTT	CTGCTGCGTG	500
	GTATCAAACG	TGAAGAAATC	GAACGTGGTC	AGGTACTGGC	TAAGCCGGGC	550
	ACCATCAACC	CGCACACCAA	GTTCGAATCT	GAAGTGTACA	TCTGTCCAA	600
40	AGACGAAGGC	GGCCGTCACA	CTCCGTTCTT	CAAAGGCTAC	CGTCCGCAGT	650
	TCTACTTCCG	TACTACTGAC	GTGACTGGCA	CCATCGAATC	GCCGGAAGGC	700
	GTAGAGATGG	TAATGCCGGG	CGACAAACATC	AAAATGGTTG	TTA	743

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *rhinoscleromatis*
- (B) STRAIN: ATCC 13884

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CCGAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	GAGATGGAAG	150
5	TTCGTGAACT	RCTGTCTCAG	TACGATTTC	CGGGCGACGA	CACCCCGATC	200
	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAACCTGGCTG	GCCACCTGGA	TACCTATATC	CCGGAACCAG	300
	AGCGTGCAT	TGACAAGCCG	TTCCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	400
10	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAA	ACCGCGAAAA	450
	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAACGCCGG	CACCATCAAC	CCGCACACCA	600
	AGTTCGAACATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	CGGCCGTAC	650
15	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAATGGTT	GTTACCTGA	TCCATCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTCGCAA				819

20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCCTTA	CATCATCGTG	100
40	TTCCTGAACA	AATGYGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGCTCTA	GTACGATTT	CCAGGCCGACG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGATGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAACGTGCTA	TCGATAAGCC	GTTCCTGCTG	CCAATCGAAG	350
45	ACGTATTCTC	CATCTCCGGT	CCTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAA	550
	CGTGAAGAAA	TCGAACCGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCTATCAA	600
50	GCCGCACACC	AAGTTCGAAT	CTGAAGTGT	CATTCTGTCC	AAAGACGAAG	650
	GC GGCGGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTCTACTTC	700
	CGTACTACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GC GTTGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA	CC		832

55

2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera cryocrescens*
 10 (B) STRAIN: ATCC 33435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

15	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCCGCCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCAG	TTGATAAGCC	GTTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCAG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGG	AACGTTGGT	TTCTGCTGCG	TGGTATCAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTGAAAT	CTGAAGTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAAACA	TCAAAATGGT	TGTTACCCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 45 (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAACCTTC	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCCCTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTGCG	TGTAGAACGC	400
	GGTATCATCA	AAAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCCTTGAAT	GTCCCGAAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAACGT	550

	GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC	600
	GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG	650
	GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT	700
5	ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TTGAGATGGT	750
	AATGCCGGGC GACAACATCA AAATGGTTGT TACCCCTGATC CACCCGATCG	800
	CGAAGGACGA AGGTCTGCGT TTCGCA	826

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus casei* subsp. *casei*
- (B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25	GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACATATCT TACTTCACG	50
	TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG	100
	TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA	150
	TTAACTGAAT ATGAATTCCC TGGCGATGAC ATTCCCTGAA TCAAAGGTT	200
30	AGCTCTTAAA GCACTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG	250
	AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT	300
	GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG	350
	TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG	400
	ACGAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA	450
35	ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA	500
	CAACATTGGC GCACTTCTAC GTGGTGTGTC TCGTGAAGAT ATCCAACGTG	550
	GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAA	600
	GCTGAAACTT ATGTTTTAAC TAAAGAAGAA GGTGGACGTC ACACCTCATT	650
40	CTTCAACAAAC TACCGCCCCAC AATTCTATTT CCGTACTACT GACGTAAC	700
	GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC	750
	ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC	800
	TAA	803

45

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
- (B) STRAIN: ATCC 19435

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

	CGGTGCAATC	CTCGTTGTTG	CTGCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAACACAT	CTTGCTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
	TTCCTTAACA	AGGCTGACCT	TGTTGATGAT	GAAGAATTGA	TGGAACTCGT	150
5	TGAAATGGAA	GTTCGTGACC	TCTTGAGCGA	ATACGACTTC	CCAGGTGACG	200
	ATATTCCGT	AATCGCTGGT	TCAGCACTTG	GTGCTTGAA	CGGTGAACCA	250
	CAATGGGTTG	CTAAAGTTGA	AGAATTGATG	GACATCGTTG	ATGAATACAT	300
	CCCAACTCCA	GAACCGGACA	CTGACAAACC	ACTCCTCTT	CCAGTCGAAG	350
	ACGTATTCTC	TATCACTGGT	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAA	400
10	CGTGGTACTG	TTAAAGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	AGAAAACATAA	AAAGCTGTTG	TTACTGGTAT	CGAAATGTTC	CGTAAAACAC	500
	TTACTGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCACTTCT	CCGTGGTATC	550
	CAACGTGACG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAC	CAGGTTCAAT	600
15	CACTCCACAC	AAACTTTCG	AAGGTGAAGT	TTACGTATTG	AGCAAAGAAG	650
	AAGGGCGGACG	TCACACTCCA	TTCTTCGACA	ACTACCGTCC	TCAATTCTAC	700
	TTCCACACAA	CTGACGTTAC	TGGTTCAAGT	AAACTTCCAG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTGCATAT	CGACGTTGAA	TTGATCCACC	800
	CAGTTGCGAT	CGAACAAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leclercia adecarboxylata*
- (B) STRAIN: ATCC 23216

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCCTTC	ATCATCGTGT	100
40	TCCTGAACAA	ATGCCACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	150
	GAGATGGAAG	TTCGTGAACT	YCTGTCCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCAATC	GTTCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGA	GAAAATCATC	GARCTGGCTG	GCTACCTGGA	TTCCTACATC	300
	CCAGAGCCAG	AGCGTGCAGT	TGACAAGCCG	TTCCCTGCTGC	CTATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAARGTTGGC	GAAGAAAGTTG	AAATCGTTGG	TATCAAGGAC	450
	ACTGCTAAGT	CTACCTGTAC	CGGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CTAACGCCAGG	CTCYATCAAG	600
50	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCCTGTCYA	AAGACGAAGG	650
	CGGCCGTAT	ACTCCGTTCT	TCAAAGGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACKACTGA	CGTGACCGGT	ACCATCGARC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GCGACAAACAT	CAAATGGTT	GTTACCTGA	TCCACCCAAT	800
	CGCAATGGAC	GATGGTCTGC	GTTC			824

55

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella micdadei*
- (B) STRAIN: ATCC 33218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

15	CGGAGCGATA TTAGTAGTAT CAGCAGCGGA TGGCCCAATG CCTCAAACGA	50
	GAGAGCACAT ACTYTTATCC CGSCAGGTAG GTGTTCCCTA TATAGTAGTG	100
	TTCTTAAACA AAGCTGACAT GGTGGATGAT GCGGAGTTAT TAGAATTAGT	150
	TGAAATGGAA GTACGCGAYT TGTTGAGCAG CTATGAATTT CCAGGAGATG	200
	AGATCCCAGAT TGTAGTTGGT TCAGCATTAA AAGCATTGGA AGGCATAACG	250
	AGTGATATAG GTGTACCAGC GATTGAGAAG TTAGTTGAGA CGATGGATTC	300
20	TTATATACCT GAGCCGGTAA GAAACATCGA TAAAAGTTTC TTGTTACCGA	350
	TCGAAGACGT GTTCTCAATA TCTGGACGAG GAACAGTAGT AACAGGACGT	400
	ATCGAAAGCG GGATCATCAA AGTTGGTGGAG GAAGTCGAGA TTGTTGGTAT	450
	ACGTGACACT CAAAAGACGA CATGCACAGG CGTTGAAATG TTCCGTAAAT	500
	TACTTGACGA AGGTCGAGCT GGAGACAAACG TTGGTATATT GCTACGTGGT	550
25	ACGAAGCGGG ATGAAGTTGA ACGCGGACAA GTATTAGCTA AGCCGGGAAAG	600
	CATTAAACCG CATACTAAAT TTGAAGCTGA AGTGTATGTG TTGTCAAAAG	650
	ATGAAGGTGG ACGTCATACC CCATTCTTA ACGGATATCG GCCTCAATT	700
	TACTTCAGGA CCACAGACGT AACTGGTTCT TGTGATTAC CTGARGGTAT	750
	AGAAATGGTA ATGCCAGGTG ATAACGTCAA GCTGATTGTT AGCTTACACT	800
30	CACCGATTGC TATGGACGAA GGTTTGCCTT TTGCAATC	838

2) INFORMATION FOR SEQ ID NO: 112

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
- (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA CTGGTTGTAT CAGCAGCTGA TGGTCCTATG CCACAAACGA	50
	GGGAACACAT TCTATTGTCT CGCCAGGTAG GTGTTCCATA TATTGTTGTG	100
	TTCATGAACA AAGCGGATAT GGTTGATGAC CCTGAGTTAT TAGAGTTAGT	150
	GGAAATGGAA GTGCGAGATT TATTAAGCAG TTACGATTTC CCAGGGGATG	200
	ACATACCTAT TGTTGTTGGT TCAGCTTGA AAGCATTGGA AGGTGAAGAC	250
55	AGTGATATAG GCGTTAAGGC TATTGAGAAA TTGGTTGAAA CAATGGATTC	300
	ATACATTCCT GAGCCAGTTA GAAACATAGA CAAGCCATT TTGTTGCCGA	350
	TTGAAGACGT ATTTCAATT TCTGGACCGC GAACAGTGTT AACTGGTCGT	400
	GTAGAGAGTG GAATTGTTAA AGTTGGTGGAG GAAGTTGAAA TTGTTGGAAT	450
	AAGAGACACC CAAAAGACGA CTTGTACGGG TGTGAGATG TTCCGTAAAT	500
60	TACTTGATGA AGGTCGAGCT GGTGATAACG TTGGTGTGTT ATTACGAGGT	550

	ACGAAGCGAG ATGAAGTGGG GCGTGGACAG GTATTGGCGA AGCCAGGAAC	600
	CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG	650
	AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATAACCG TCCACAATTC	700
5	TATTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT	750
	TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG	800
	CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT	838

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
- (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25	GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC	50
	GAGCACATCC TGCTGGTCG TCAGGTTAGGC GTTCCGTACA TCATCGTATT	100
	CCTGAACAAG TCGGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG	150
	ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC	200
30	ACTCCGGTAG TCCCGGGTTC AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA	250
	GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC	300
	CAGAACCTGA GCGTGGCATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC	350
	GTATTCTCTA TCTCCGGCCG TGGTACCCTT GTTACCGGTC GTGTAGAGCG	400
	CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCGGT ATCAAAGATA	450
35	CCACCAAGAC CACCTGTACC GGC GTTGAAA TGTTCCGTAA GCTGCTGGAC	500
	GAAGGCCGTG CGGGCGAGAA CGTGGGC GTT CTGCTGCGCG GTACCAAGCG	550
	TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC	600
	CTCACACCCA GTTCGTGTCA GAA GTGTATA TCCTGAGCAA GGATGAAGGC	650
	GGCCGTATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG	700
40	TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAAGGC GTAGAGATGG	750
	TAATGCCAGG CGACAAACATT CAGATGACCG TAAGTCTGAT TGGCGCCGATC	800
	GCAATGGACG AAGGTCTGCG CTTCGCAA	828

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2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Leminorella richardii</i>
	(B) STRAIN: ATCC 33998

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

	GCTATCCTGG	TTGTTGCTGC	GAUTGACCGGC	CCAATGCCTC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTGCGCC	AGGTAGGC GT	TCCTTACATC	ATCGTGTTC	100
	TGAACAAGTG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
5	ATGGAAGTTC	GTGAACCTCT	GTCTCAATAC	GACTTCCC GG	GCGACGATAC	200
	GCCGGTTGTT	CGCGGTTCA G	CGCTGAAGC	GCTGGAAAGGT	GACGCGYAGT	250
	GGGAARCGAA	AATCATTGAA	CTGGCGGAAT	CCTTRGATAC	TTAYATTCCA	300
	GAGCCAGAGC	GTGCGATTGA	CAAGCCGTT C	CTGCTGCTA	TCGAAGACGT	350
	TTTCTCTATC	TCTGGCCGTG	GTACTGTAGT	CACCGGT CGT	GTAGAGCGCG	400
10	GCATCATCAA	AGTTGGTGAA	GAAGTGGAAA	TCGTGGGAAT	CAAAGACACC	450
	ACCAAGACCA	CCTGTACTGG	CGTTGAAATG	TTCCGTAAGC	TGCTGGACGA	500
	AGGCCGTGCA	GGTGAGAACG	TTGGTGTCT	GCTGCGYGGT	ACTAAGCGTG	550
	ACGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCAGGCAC	CATCACTCCT	600
	CACACAGAAT	TCGTGTCAGA	AGTGTATATC	CTGAGCAAGG	ATGAAGGCGG	650
15	YCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCTCAGTTC	TACTTCCCGTA	700
	CGACTGACGT	GACC GG CACC	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	750
	ATGCCAGGCG	ATAACATCCA	GATGGTAGTT	ACGCTGATTG	CCCCAATCGC	800
	GATGGACGAA	GGTCTGCGCT	TCGCAA			826

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2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leptospira interrogans*
- (B) STRAIN: ATCC 23581

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

	TGCGGCGATT	CTTGTAGTAT	CCGCAACTGA	CGGACCTATG	CCACAAACAA	50
	AAGAACATAT	CCTTCTTGCT	CGTCAGGTAG	GTGTTCCATA	TGTAATTGTA	100
40	TTCATTAACA	AAGCAGATAT	GCTTGCTGCT	GACGAAAGAG	CAGAAATGAT	150
	CGAAATGGTT	GAGATGGACG	TCGTGAACT	TCTCAATAAG	TATAGCTTCC	200
	CAGGAGATAC	AACTCCATAC	GTTCATGGIT	CTGGGGTAAA	AGCACCTTGAG	250
	GGCGATGAAT	CTGAAATTGG	GATGCCTGCA	ATTCTCAAAT	TGATGGAAGC	300
	TCTGGATACT	TTCTTCCAA	ATCCAAAACG	TGTAATCGAC	AAACCTTTCC	350
45	TTATGCCAGT	AGAACAGCTT	TTCTCGATCA	CTGGTCGTGG	AACTGTTGCA	400
	ACTGGAAAGAG	TGGAACAAGG	TGTTTTGAAA	GTGAACGACG	AAGTTGAAAT	450
	TATCGGTATC	CGCCCAACAA	CAAAAACTGT	TGTTACCGGT	ATCGAAATGT	500
	TCAGAAAACT	TCTCGATCAA	GCGGAAGCTG	GCGACAACAT	CGGCGCTCTT	550
	CTTCGTGGAA	CTAAAAAAGA	AGAAATCGAA	AGAGGGCAAG	TTCTTGC GAA	600
50	GCCAGGTTCT	ATCACTCCTC	ACAAAAAGTT	TGCCGCTGAG	G TGTATGTAT	650
	TAACTAAGGA	TGAAGGCGGA	CGTCATACTC	CGTTTATCAA	TAACTACCGT	700
	CCTCAGTTTT	ACTTTAGAAC	AACTGACGTA	ACCGGAGTTT	GTAACCTTCC	750
	TAATGGTGTG	GAAATGGTTA	TGCCTGGTGA	TAACGTTTCT	TTGACGGTTG	800
	AATTGATTAG	CCCGATCGCA	ATGGACAAAGG	GTCTTAAGTT	CGC	843

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2) INFORMATION FOR SEQ ID NO: 116

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Megamonas hypermegale*
- (B) STRAIN: ATCC 25560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

15	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACCTTC	TCGAACATTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTACAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAACTGGTAT	CGAAATGTTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTACTA	CTGACGTTAC	TGGTGTGTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mitsuokella multacida*
- (B) STRAIN: ATCC 27723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCG	ATGAGTACAT	300
	CCCGACGCCG	GTCCGCGACA	ACGCTAACGCC	GTTCCTGATG	CCGGTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCCT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTC	CGCAAGATGC	500
60	TTGATTTCGC	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

	GACCGCAAGG	AGATCGAGCG	TGGCCAGGTT	CTCGCAAAGC	CGGGCACGAT	600
	TCATCCGCAC	ACGAAGTTCA	AGGCTCAGGT	CTATGTCTG	ACGAAAGAAG	650
	AAGGCCGGCG	TCATACGCCG	TTCTTCACGA	ACTATGCC	GCAGTTCTAC	700
5	TTCCGCACGA	CGGACGTAAC	TGGCGTAGTC	AAACTGCCG	AAGGCACGGA	750
	GATGGTTATG	CCTGGCGATA	ACGTCGAGAT	GGAAGTTGAG	CTCATCACCC	800
	CGATCGCTAT	CGAGAAGGGC				820

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mobiluncus curtisi* subsp. *holmesii*
- (B) STRAIN: ATCC 35242

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

	CGGCGCTATC	CTCGTGGTGG	CTGCTACTGA	CGGTCCGATG	GCTCAGACCA	50
	AGGAACACAT	CCTGTTGGCT	AAGCAGGTTG	CGGTGCCCTC	CATCCTGGTC	100
	GCTCTGAACA	AGTGCGATTG	TTCCGATGTG	GACGAAGACA	TGCTCGAAAT	150
	CGTCGAGGAC	GAAATCCGCG	ATGACCTGGA	GAAGCAGGGC	TTCGATCGTG	200
30	ACTGCCCGAT	TATCCACGTT	TCGCTCTGA	AGGCCCTGGA	AGGCAGCCCC	250
	GAGTGGACCA	AGAAGATTGA	AGAGCTCATG	GAAGCGGTCG	ATACCTACAT	300
	TCCTGAGCCT	GTTCGTGACC	TCGACAAGCC	GTTCTTGATG	CCTATCGAAG	350
	ACGTCTTCAC	CATTACTGGT	CGCGGTACCG	TAGTGACCGG	TCGTGTGGAA	400
	CGCGGCAAGC	TACCGTTGAA	CGCCGAAGTG	GAAATCGTAG	GTATTCGTCC	450
35	TACGCAAAAG	ACCACCGTTA	CCGGTATCGA	AATGTTCCAC	AAGTCCATGG	500
	ACGAAGCCTA	CGCCGGCGAG	AACTGTGGTC	TGTTGCTGCG	TGGCACCAAG	550
	CGTGAGGACG	TTGAGCGCGG	TCAGGTTGTC	TGCATTCTG	GCTCCGTGAC	600
	CCCGCACACC	AAGTCGAGG	GCAAGGTCTA	CATCTTGAAG	AAGGACGAAG	650
40	GTGGACGTCA	CAAGTCGTTC	TACGACGGCT	ACCGCCCGCA	GTTCTTCTTC	700
	CGCACCAACG	ACGTGACCGG	TGTTATTACAC	CTGCCCGAAG	GCACCGAAAT	750
	GGTTATGCCT	GGCGACACCA	CCGAAATTAG	CGTTGAGCTG	ATTCAAGCCTA	800
	TCGCTATGGA	GGAAGGTCTC	GGCTTCGCTA	T		831

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2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
- (B) STRAIN: ATCC 35017

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

	GGTGCAATT	TGGTTGTG	TGCAACTGAT	GGCCCTATGC	CACAGACTCG	50
	TGAGCACATC	CTGTTAGGT	GTCAGGTTGG	CGTTCCATAC	ATCATCGTT	100
5	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAGCTGTT	AGAACTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTAG	TACGATTCC	CAGGCGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCTCTGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATT	GAACTGGCAG	AAGCACTGGA	TTCTTATATC	300
	CCAGAGCCAG	AGCGTGACAT	TGATAAGCCA	TTCCTGTTAC	CAATCGAAGA	350
	CGTATTCTCA	ATTTCAGGCC	GTGGTACAGT	TGTTACTGGT	CGTGTGAGC	400
10	GTGGTATCGT	TAAAGTCGGT	GAAGAAGTTG	AAATCGTTG	TATCAAAGAT	450
	ACCGTGAAAAA	CAACATGTAC	TGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAC	550
	GTGATGATAT	CGAACGTGGT	CAAGTATTGG	CTAAACCAGG	TTCAATCACT	600
15	CCGCATACAA	CTTTCGAATC	AGAAGTTAC	ATCCTGAGCA	AAGATGAAGG	650
	TGGCCGTCAT	ACTCCATTCT	TCAAAGTTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GTGATAACAT	CAAAATGATC	GTTAECTCTGA	TCCACCCAAT	800
	TGCAATGGAT	GCAGGTCTGC	GT	TTT		825

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2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:

25	(A)	LENGTH:	827 bases
	(B)	TYPE:	Nucleic acid
	(C)	STRANDEDNESS:	Double
	(D)	TOPOLOGY:	Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A)	ORGANISM:	<i>Branhamella catarrhalis</i>
(B)	STRAIN:	ATCC 43628

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

	TGGTGCTATC	TTGGTTGTTT	CTGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCATAT	CCTACTATCT	CGTCAGGTTG	GTGTACCATA	CATCATGGTA	100
40	TTCATGAACA	AGTGCGATAT	GGTTGATGAT	GAAGAGCTAC	TAGAATTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTATCTGA	CTATGATTT	CCTGGTGATG	200
	ATACCCCAAT	CATCAAAGGT	TCAGCACTAG	AAGCATTTGAA	TGGTCTGTAT	250
	GGTAAATATG	GCGAGCCTGC	AGTTCTAGAA	CTGCTAGACA	CACTAGACAG	300
45	CTATATCCC	GAGCCTGAGC	GTGATATCGA	TAAGTCATT	TTGATGCCAA	350
	TTGAAGATGT	CTTCTCGATC	TCAGGTCGTG	GTACAGTTG	GACTGGTCGT	400
	GTTGAATCAG	GTATTATTAA	AGTTGGTGT	GAAATTGAAA	TCATCGGTAT	450
	CAAACCAACT	GCTAAAACCA	CCTGTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	TGTTAGACGA	AGGTCGTGCA	GGTGAGAACT	GTGGTATCTT	GTTGCGTGGT	550
50	ACTAAGCGTG	AAGAAGTTCA	ACCGGGTCAA	GTACTTGCAA	AACCAGGTT	600
	AATCACCCCCA	CATACTAAGT	TTGATGCTGA	AGTTTATGTA	CTGTCAAAAG	650
	AAGAAGGTGG	TCGTACACCC	CCATTCTAA	ATGGCTATCG	CCACACAGTTC	700
	TACTTCCGTA	CCACAGATGT	GACTGGTGCC	ATCACTCTAC	AAGAAGGTAC	750
	CGAAATGGTT	ATGCCTGGTG	ACAATGTTGA	GATGAGTGT	GAGCTTATCC	800
	ACCCAAATCGC	CAGGATAAAAG	GTCTACG			827

55

2) INFORMATION FOR SEQ ID NO: 121

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
- (B) STRAIN: ATCC 25830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

15	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCCTTA	CATCATCGTA	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAACTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCAGGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAACCTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGGCC	GTTCCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTGAA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCCAG	GTTCAATCAA	600
	ACACACAYACC	AAATTGAAAT	CAGAAGTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTG	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACACACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGAT	CGTCACCCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: TB 299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

50	GGTGCATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGGAGCT	GCTGGCTGCC	CAGGAATTG	ACGAGGACGC	200
	CCCAGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACCGAAGT	250
55	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTT	CTGATGCCGG	TCGAGGACGT	350
	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCAGGGCGACA	ACGTTGGTT	GCTGCTGCCG	GGCGTCAAGC	550

	5	GCGAGGACGT CGAGCGTGGC CAGGTTGTCA CCAAGCCGG CACCACCAAG 600
		CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
		CGGCCGGCAC ACGCCGTTCT TCAACAACTA CCGTCCGCAG TTCTACTTCC 700
		GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG 750
10	GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT 800	
		CGCCATGGAC GAAGGTCTGC GTTTC 825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
- (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC TTGGTATGTT CCGCAGCTGA CGGTCTATG CCGCAAACTC 50
	GCAGAACACAT CCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTG 100
	TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAGCTGT TGGAGCTGGT 150
	TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGTGACG 200
30	ACTGCCGAT CGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGACGCA 250
	GCTTACGAAG AAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
	CCCAACACCT GAGCGTGCAG TGGACAAACC TTTCTTGTG CCTATCGAAG 350
	ACGTATTCTC TATTTCCGGT CGCGGTACAG TAGTAACCGG TCGTGTAGAG 400
	CGCGGTATCA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
35	AACTCAAAAA ACCACTTGT A CCGGTGTTGA AATGTTCCGC AAAC TGCTGG 500
	ACGAAGGTCA AGCTGGTGAC AACGTAGGTG TATTGCTGCG TGGTACTAAA 550
	CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACTATCAC 600
	TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
40	GTGGTCGTCA CACTCCGTTC TTCGCTTAAC ACCGTCCACA ATTCTACTTC 700
	CGTACTACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
	GGTAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
	----- TCGCTA 806

45 2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
- (B) STRAIN: ATCC 25295

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

	CGGCGCAATC	TTGGTATGTT	CCGCTGCYGA	CGGTCTATG	CCGCAAAC	TC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	CGGTACCTTA	CATCATCGTG		100
	TTCATGAATA	AATGCGACAT	GGTTGAYGAT	GCCGAAC	TGGAAC	TGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG		200
	ACTGCCGAT	CGTACAAGGT	TCCGCACTGA	AAGCCTTGG	AGGCGACGCA		250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCTGCATTGG	ACAGCTACAT		300
	CCCGACACCT	GAGCGTGC	TGGACAAACC	GTTCTGTTG	CCTATCGAAG		350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACAG	TAGTAACC	TCCGTG	TAGAG	400
10	CGCGGTATCA	TCCACGTCGG	TGACGAGATC	GAAATCGTAG	GTCTGAA	AGA	450
	AACCCAAAAA	ACCACTGT	CCGGTGTG	AATGTTCCGC	AAACTG	CTGG	500
	ACGAAGGTCA	AGCAGGTGAC	AACTGAGGCG	TATTGCTGCG	CGGTAC	CAAA	550
	CGTGAAGAAG	TGGAACCGG	TCAAGTATTG	GCTAAACC	GTAC	CATCAC	600
	TCCTCACACC	AAATTCAAAG	CAGAAGTTA	CGTATTGAGC	AAAGAAG	AGG	650
15	GTGGTCGTCA	TACTCCGTT	TTCGCTAA	ACCGTCCACA	ATTCTACTTC		700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAG	AAAT	750
	GGTTATGCCT	GGTGAGAACG	TGGCCATCAC	TGTAGAACTG	ATTGCAC	CTA	800
	TCGCTATGGA	AGAAGGTCTG	CG				822

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2) INFORMATION FOR SEQ ID NO: 125

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
- (B) STRAIN: ATCC 13120

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

	CGGCGCGACT	TGGTATGTT	CGCAGCTGAC	GGTCCTATGC	CGCAAAC	CCG	50
	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT		100
40	TCATGAACAA	ATGCGACATG	GTAGACGATG	CCGAGCTGTT	GGAAC	TGGTT	150
	GAAATGGAAA	TTCGTGACTT	GTGTC	TAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTT	TGGAA	GGTGATGUTG	250
	CTTACGAAGA	AAAAAATCTT	GAATTGGCTG	CTG	CCTTGG	GA CAGCTACATC	300
	CCAACACCTG	AGCGTGTGT	GGACAAACCT	TTCTT	GTTGC	CTATCGAAGA	350
45	CGTATTCTCT	ATCTCTGGTC	GTGGTACAGT	AGTAACC	GGT	CGCGTAGAGC	400
	GCGGTATCAT	CCACGTGGT	GACGAGATCG	AAATCG	AGG	TCTGAAAGAA	450
	ACTCAAAAAA	CCACTTGTAC	CGGC	GTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCAGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGT	ACTAAAC	550
	GTGAAGACGT	AGAGCGTGGT	CAAGTATTG	CTAAACC	AGG	TACCATCACT	600
50	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAG	AGGG	650
	TGGTCGTAC	ACTCCATT	TCGCTAA	CCGTCC	CACAA	TTCTACTTCC	700
	GTACTACCGA	CGTA	ACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTG	TTGCG	CCAAT	800
	CGCTATGGAA	GAAGTCTGCG					820

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2) INFORMATION FOR SEQ ID NO: 126

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
- (B) STRAIN: ATCC 49226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

15	GGTGCAATCC	TGGTATGTTC	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGGATG	CCGAGCTGTT	GGAACTGGTT	150
	GAAATGGAAA	TCCCGCACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGAA	GGCGATGCCG	250
20	CTTACGAAGA	AAAAATCTTC	GAAC TG GCTA	CCGCATTGGA	CAGCTACATC	300
	CCGACTCCCG	AGCGTGCCTG	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTCTCC	ATTTCGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
25	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCCT	ATTGCTGCCG	GGTACCAAAC	550
	GTGAAGACGT	AGAACCGGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
30	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
	CGCTATGGAA	GAAGGTCTGC	GCTTGGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
- (B) STRAIN: ATCC 23970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGCGCGAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGGAT	GCCGAGCTGT	TGGAACTGGT	150
	TGAAATGGAA	ATCCCGGACC	TGCTGTCAAG	CTACGACTTC	CCAGGGCGACG	200
	ACTGCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAAATCTT	CGAAC TG GCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCTG	TGGACAAACC	GTTCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
60	AACCCAAAAA	ACCACCTGTA	CCGGTGTGCA	GATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCAGGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAA	550

	CGTGAAGAAG	TGGAACGCGG	TCAGGTATTA	GCCAAACCGG	GTACCACATCAC	600
	TCCGCACACC	AAGTTCAAAG	CAGAAGTGT	TGTATTGAGC	AAAGAAGAGG	650
	GCGGTCGTCA	CACTCCGTTC	TTCGCCAACT	ACCGTCCGCA	ATTCTACTTC	700
5	CGTACCAACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GCGTGAAAT	750
	GGTAATGCC	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
	TCGCTATGGA	AGAAGG				816

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: ATCC 13077

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

	CGGTGCAATC	CTGGTATGTT	CCGCAGCCGA	CGGTCTATG	CCGCAAACCC	50
	GCGAACACAT	CCTGCTGGCC	CGTCAAGTAG	CGGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTCGACGAT	GCCGAGCTGT	TGGAACTGGT	150
	TGAAATGGAA	ATCCCGGACCC	TGCTGTCCAG	CTACGACTTC	CCCGGCGACG	200
30	ACTGCCGAT	CGTACAAGGT	TCCGCACTGA	AAGCCTTGGGA	AGGCATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	TTTCTTGTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTCGG	TGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
35	AACTCAAAAA	ACCACTTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACAATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GCGGCCGCCA	TACCCCGTTC	TTCGCCAACT	ACCGTCCCCA	ATTCTACTTC	700
40	CGTACCAACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GCGTGAAAT	750
	GGTAATGCCG	GGCGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCGCCTA	800
	TCGCTATGGA	AGAAGGTTTG	CGCTTTGCGGA	T		831

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2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
- (B) STRAIN: ATCC 19696

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

	CGGCGCAATC	TTGGTATGTT	CTGCTGCYGA	CGGTCTATG	CCGCAAACCC	50
	GYAACACAT	CCTGTTGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAACTGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYACG	200
	ACTGCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGA	AGGCATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCCTGTTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
10	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACATGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAA	550
	CGTGAAGAAG	TGGAACGC GG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGT	CGTATTGAGC	AAAGAAGAGG	650
15	GTGGTCGTCA	TACTCCGTT	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAAYG	TAGCCATYAC	TGTAGAACTG	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
- (B) STRAIN: ATCC 9913

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	40	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	150
		GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	200
		CTGCCCCATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGAA	250
		CTTACGAAGA	AAAAATCTTC	GAACCTGGCTG	CTGCATTGGA	300
		CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCCTGTTGC	350
45		CGTATTCTCC	ATCTCCGGTC	GGGGTACCGT	AGTAACCGGC	400
		GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	450
		ACCCAAAAAA	CCACTTGTAC	CGGTGTTGAA	ATGTTCCGCA	500
		CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	550
		GTGAAGAAGT	GGAACCGGGT	CAAGTATTGG	CTAAACCGGG	600
50		CCTCACACTA	AATTCAAAGC	AGAAGTTAC	GTATTGAGTA	650
		TGGTCGTCA	ACTCCGTTCT	TCGCTAACTA	CCGTCTCAA	700
		GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TTGGAAGAAGG	750
		GTTATGCCTG	GTGAGAACGT	AGCCATCACT	TGTAGAAATG	800
		CGCTATGGAA	GAAGGTCTGC	GCTTTGC	TTGCACCGAT	829

55

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
- (B) STRAIN: ATCC 14221

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

15	CGGCGCGACT	TGGTATGTTC	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGTT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGTCTG	GGACAAACCT	TTCTTGTTC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGCGTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCCT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCAATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
- (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

50	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTGAAAGC	TTTGGAAAGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTGA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCCTGAGC	GYGCTGTTGA	TAAACCATT	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCTG	GTAGAGCGCG	400
	GTATTATTCA	CGTAGGGCGAT	GAAATTGAAA	TTGTAGGTT	GAAAGARACY	450
	CAAAAAAACTA	CTTGTACCGG	CGTTGAAATG	TTCCGTAAT	TGCTGGATSA	500
60	AGGTCAAGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550

	AAGACGTTGA GCGTGGTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG	600
	CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCCG	650
	TCGTCATACT CCGTTCTTCG CTAACATATCG TCCGCAATT C TATTCCGTA	700
5	CTACAGACGT TACCGGTGCK GTRACTTAG AAGAAGGTGT GGAAATGGTA	750
	ATGCCTGGTG AGAACGTTGC CATTACTGTW GARYTGATYGC CTCCGATTGC	800
	KATGGAAGAA GGYTGCCT	818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
- (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25	CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTCGCT CGTCAGGTTG CGGTTCCGGC AATCGTCGTG	100
	TTCCTGAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT	150
	TGAACCTGGAA GTTCGCGAAC TTCTGTCGAA ATACGATTT CCGGGCGACG	200
30	AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG	250
	AAGGAACTGG GCGAAGACGC CGTTCGTTCG CTGATGGCCG CTGTTGACGA	300
	CTACATTCCG ACCCCCGAAC GTCCGATCGA CCAGCCGTT CTGATGCCGA	350
	TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCGC	400
	GTTGAGCGCG GTATCGTCAA GGTTGGTCAA GAAGTTGAAA TCGTCGGCAT	450
35	CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC	500
	TGCTCGAYCA GGGCCAGGCT GGCGACAACA TCGGCGCTCT GATCCGCGGC	550
	GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTC	600
	TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG	650
40	ACGAAGGTGG CCGTCATACG CCGTTCTTA CGAACTACCG TCCGCAGTTC	700
	TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC	750
	GGAAATGGTT ATGCCTGGCG ACAACGTCGC TATGGACGTC ACCCTGATCG	800
	TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA	836

45 2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
- (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

	CCTGGTTGTT	GCTGCGACTG	ATGGCCCAAT	GCCACAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTT	GGCGTTCCCTT	ACATCATCGT	GTTCCCTGAAC	100
	AAGTGTGACA	TGGTTGATGA	TGAAGAGCTG	CTGGAACCTGG	TAGAGATGGA	150
5	AGTACGTGAC	CTGCTGTAC	AGTACGACTT	CCCAGGCGAT	GACACCCCCGA	200
	TCGTTCTGGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCCTTCC	TGAGTGGGAA	250
	GCAAAAATCG	TTGAGCTGGC	TGAACACCTG	GACAACATACA	TCCCGGATCC	300
	AGTCCGTGCG	ATCGACATGC	CGTTCCCTGCT	GCCAATCGAA	GACGTATTCT	350
	CAATCTCTGG	CCGTGGTACCG	GTTGTTACCG	GTCGTGTTGA	GCGCGGCATC	400
10	GTAAAGTCG	GCGACGAAGT	TGAAATCGTG	GGTATCAAAG	ATACTGCGAA	450
	ATCAACCTGT	ACCGGTGTTG	AGATGTTCCG	TAAGCTGCTG	GACCAGGGTC	500
	AGGCAGGCAGA	AAACTGTTGGT	GTTCTGCTGC	GCGGTATCAA	GCGTGAAGAC	550
	ATCCAGCGTG	GCCAGGTTCT	GGCTAACCCA	GGCTCAATCA	AGCCGCACAC	600
	CCAGTTCGAG	TCAGAAAGTT	ACGTTCTGTC	TAAAGACGAA	GGTGGCCGCC	650
15	ATACTCCGTT	CTTCAAAGGC	TATCGTCCAC	AGTTCTACTT	CCGTACAAC	700
	GATGTAACCG	GTTCAGTAGA	GCTGCCAGAA	GGCGTTGAGA	TGGTCATGCC	750
	AGGCGACAAC	ATCAAAATGG	TTGTTACCCCT	GATCCACCCA	ATCGCAATGG	800
	ACGAA					805

20

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

	CGCGATCTG	GTTGTTGCTG	CGACTGATGG	CCCAATGCCCT	CAGACCCGTG	50
	AGCACATCCT	GCTGGGCCGT	CAGGTTGGCG	TTCCTTACAT	CATCGTGTTC	100
40	CTGAACAAGT	GTGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	GATGGAAGTT	CGCGATCTGC	TGTCTCAGTA	CGACTTCCCA	GGCGACGATA	200
	CCCCAACATCGT	ACGCGGTTCT	GCGCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
	TGGGAAGCGA	AAGTCGTTGA	GCTGGCTGGT	CACCTGGATA	CTTACATTCC	300
	AGATCCAGTA	CGTGCTATCG	ATCTGCCGT	CCTGCTGCCA	ATCGAAGACG	350
45	TATTCTCAAT	CTCTGCCGT	GGTACCGTTG	TTACCGGTG	TGTTGAGCGC	400
	GGCATCGTGA	AAGTGGCGA	CGAAGTAGAA	ATCGTTGGTA	TCAAAGCGAC	450
	TGCCCAAGTCT	ACCTGTACCG	GTGTTGAAAT	GTCCCGAAA	CTGCTGGAC	500
	AGGGTCAGGC	AGGCGAGAAC	TGTGGTGTTC	TGCTGCGCGG	TATCAAGCGT	550
	GAAGAGATCC	AGCGTGGTCA	GGTTCTGGCT	AAGCCAGGCA	CCATCAAGCC	600
50	ACACACCAAG	TTCGTATCAG	AAGTGTACGT	ACTGTCTAAA	GACGAAGGCG	650
	GCCGTCTAC	TCCGTTCTTC	AAAGGCTACC	GTCCACAGTT	CTACTTCCGT	700
	ACYACTGATG	TGACCGGCAM	CATMGAACGT	CCAGAAGGCG	TTGAGATGGT	750
	AATGCCAGGC	GACAACATCA	AAATGRCCGT	TGAGCTGATC	CACCCAATCG	800
	CGATGGACCA	GGGTCTGCGT	TTCGC			825

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2) INFORMATION FOR SEQ ID NO: 136

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
- (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

15	CACAAACACG	TGAGCACATC	CTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAACT	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAC	200
	GGYGTAGCTG	AGTGGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
20	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCCTTCTTC	300
	CGATTGAAGA	CGTGTCTCA	ATTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GGGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAACR	GTGAAGAAAT	CGAACGTGGT	CAAGTGTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTGTGAATC	AGAAGTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCA	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACCGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTGA	750
	TTCACCCAAT	CG				762

30

2) INFORMATION FOR SEQ ID NO: 137

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 832 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
- (B) STRAIN: ATCC 27337

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

50	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
	GAGAACACAT	CTTATTATCA	AGACAAAGTAG	GAGTACCAT	TATCGTAGTA	100
	TATTGAAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAA	TACTATCTGA	ATATGGATTC	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAA	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAACGT	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACTTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAAG	GAACAATTCA	600

5	TCCTCATACA AACTTCAGTG GAGAAAGTATA TGTATTGACA AAAGAAGAAG GAGGAAGACA TACTCCATTC TTCTCAGGAT ACAGACCACA ATTTTACTTT AGAACACACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATG ATTCAACCAA TTGCAATGGA AACAGGATTA CGATTTGCAA TT	650 700 750 800 832
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2) INFORMATION FOR SEQ ID NO: 138

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:
 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25	TAGTATGTTG AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC GTAGTAGGAT CAGCATTAAA AGCCCTAGAC GATCCAGACG GAGAATGGGG	50 100 150 200 250
30	AGACAAAATC GTAAAACATA TGGAAGMAGT AGACGAATAC ATCCCAACAC CAGTAAGAGA TACAGAACAC CCATTCTAA TGCCAATCGA AGACRTATT TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAAGGTGT AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAGCA GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA	300 350 400 450 500
35	GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGGAG TACAAAGAGA AGAAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACAC ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA AGACACACAC CATTCTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC	550 600 650 700
40	AACAGACGTA ACAGGAGACA TCCAACTAGC AGACGGAGTA GAAATGGTAA TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA ATGGACGAAG GACTAAGATT CGC	750 800 823

45 2) INFORMATION FOR SEQ ID NO: 139

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

	CTATCATCGT	AGTATCTGCA	GCAGACGGTC	CAATGCCAA	ACAGAGAGAA	50
	CACATCCTAC	TAGCAAGACA	AGTAGGCGTT	CCAAAATCG	CAGTATTCT	100
	AAACAAAGAA	GACCAAGTAG	ACGATCCAGA	ACTAATCGAA	TTAGTAGAAA	150
5	TGGAAATCAG	AGACCTACTT	TCAGAACATCG	ACTTCGATGG	AGACAACGCT	200
	CCAGTAGTAG	TAGGATCTGC	TCTTAAATCA	CTAGAAGAAG	GCGGAGAAGG	250
	CCCATGGTCA	GACAAAATCC	TTGACCTAAT	GGCACAAAGTA	GACGAATACT	300
	TCGACATCCC	AGAAAGAGAC	AACGACCAAC	CATTCTAAT	GCCAGTAGAA	350
	GACGTAAATGA	CAATCTCAGG	ACGTGGAACA	GTAGAACAG	GAAGAGTTGA	400
10	AAGAGGAACA	CTAAAAGTTG	GTGATACAGT	AGAAATCGTA	GGACTAACAG	450
	AAGATACAAA	AGAAACAGTA	GTAACTGGAG	TAGAAATGTT	CCACAAATCM	500
	CTAGACCAAG	CAGAATCTGG	AGATAACGTA	GGACTACTAC	TAAGAGGAGT	550
	AACAAGAGAT	CAAATCTCAA	GAGGACAAGT	ACTAGCAAAA	CCAGGWTCA	600
	TAAACCCACA	CACAGAATTG	GAAGGTCAAG	TATACGTACT	AACAAAAGAA	650
15	GAAGGTGGAC	GTCACACACC	ATTCTTCAGT	GGATATAGAC	CACAATTCTT	700
	CTTTAGAACAA	ACAGACGTA	CAGGAGACAT	CGAACTAGAA	GAAGGCGTAG	750
	AAATGGTAAT	GCCAGGAGAC	AACGCAACAT	TCAAAATCAC	ACTCCAAAAA	800
	CCAATCGCTC	TAGAAGAAGG	ACTAAGATTC	GC		832

20 2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
- (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

	CGGTGCTATC	ATCGTAGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAGACGC	50
	GTGAGCACAT	CCTACTAGCA	CGTCAGGTCA	ACGTACCTCG	TCTAGTTGTC	100
	TTTATGAACA	AGTGCGACCT	TGTTGATGAC	GAGGAGATGC	TCGAGCTCGT	150
40	AGAGATGGAT	ATGCGTGAGC	TACTAACGTT	CTATGACTTT	GACGGCGACA	200
	ACACTCCTGT	CATCCGTGGT	TCTGCTCTTG	GTGCTCTCAA	TGGTGAGCCT	250
	AAGTGGGTAG	AGAAGGTTAT	GGAGCTCATG	GAGGCTGTAG	ACACTTGGAT	300
	CCCACTACCT	GAGCGCGACA	TCGACAAGCC	TTTCCTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGGTACTG	TCGCTACTGG	TCGTATCGAG	400
45	ACTGGTGTG	TTAACGGTCAA	CGATGAGGTT	CAGATCATCG	GTCTAGGTGC	450
	TGAGGGTAAG	AAGAGCGTCG	TAACCTGGCGT	GGAAATGTT	CGCAAGATCC	500
	TTGATGAGGG	TGAAGCTGGT	GATAACGTAG	GTCTCCTACT	CCGTGGTATC	550
	GACAAGGACG	AGATCAAGCG	CGGTATGGTC	CTAGCACACC	CAGGTCAAGGT	600
	CAAGCCTCAC	GATCACTTCA	AGGCTGAGGT	CTATATCCTG	AAGAAGGAAG	650
50	AGGGTGGTCG	TCACACACCA	TTCCACAAACA	AGTACCGTCC	TCAGTTCTAC	700
	ATCCGTACGC	TAGACGTAAC	GGGCGAGATC	ACACTCCCAG	AGGGTGTAGA	750
	GATGGTTATG	CCTGGTGATA	ACGTCACCAT	CGATGTCAAG	CTCATCTCTC	800
	CAGTAGCTTG	TAGCGTAGGT	CTACGCTTCG	C		831

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2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: ATCC 33277

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCTATG	CCTCAGACTC	50
GCGAGCACAT	CCTTTGGCT	CGCCAGGTA	ACGTTCTCG	TCTGGTTGTT	100
15 TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
TGAAATGGAC	ATGCGCGAAC	TCCTTCTTT	CTACGATTTC	GATGGTGACA	200
ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTGAA	TGGAGAGCCT	250
CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAACCTGGGT	300
TCCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
20 ACGTGTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTT	CGTAAGATT	500
TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCAC	CGGGTAAGAT	600
25 TACTCCTCAC	AAGAGATT	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
AAGGTGGTCC	CCACACTCCT	TTCCACAAACA	AATATCGTCC	GCAGTTCTAC	700
ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
CGGTGCGATG	TAATGTAG				818

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2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
- (B) STRAIN: ATCC 49100

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

CGGCCGTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAAC	50
50 GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCAT	CATCATTTG	100
TTCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAACTGGT	150
TGAAATGGAA	GTTCGTGAGC	TTCTGTC	GTACGATTTC	CCAGGTGATG	200
ATACTCCAGT	TGTTCGTGGT	TCTGCGCTGA	AAGCGTRGA	AGGCGAAGCT	250
GAGTGGGAAG	CTAAAATCAT	TGAATTGGCT	GACTCCCTGG	AYAGCTACAT	300
55 TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
ACGTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
CGCGGTATCG	TTAAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
TACTGTGAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AARTTACTGG	500
ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
60 CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCA	GTTCAATCAA	600

	CCCGCATACT	AACTTCGTAT	CAGAACGTTA	TATCCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTG	TTCAAAGGCT	ACCGTCCACA	GTTYTACTTC	700
	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
5	GGTAATGCCA	GGTGATAACA	TTCAGATGAC	TGTAACTCTG	ATTGCCCAA	800
	TCGCGATGGA	CGAAGGTTA	CGCTTCGCTA			830

2) INFORMATION FOR SEQ ID NO: 143

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
- (B) STRAIN: ATCC 25845

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25	TGGTGCTATC	TTGGTTGTAG	CTGCTACTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAGCACGT	ATTGCTCGCT	CGTCAGGTAA	ACGTACCTCG	CTTGGTTGTA	100
	TTCTTGAACA	AGTGTGATAT	GGTTGACGAT	GCTGAGATGC	TTGACCTCGT	150
	TGAGATGGAG	GTTCGTGAGA	TCCTCGAGCA	GTACGGTTAT	GAGGAGGATA	200
	CTCCTATTAT	TCGTGGTTCT	GCACTCGGTG	CTTTGAACGG	TGTTGAGAAG	250
30	TGGGTAGACT	CTGTAATGGA	GCTCATGGAT	ACTGTTGACA	CTTGGATTGA	300
	AGAGGCCAGAG	CGTGAGATTG	ACAAGCCATT	CTTGATGCCT	GTTGAGGACG	350
	TATTCTCTAT	CACAGGTCGT	GGTACTGTAG	CTACTGGTCG	TATCGAGACT	400
	GGTATCTGTA	AGGTAGGTGA	TGAGGTTCA	TTGCTCGGTC	TCGGTGAGGA	450
	CAAGAAGTCT	GTTATCACTG	GTGTTGAGAT	GTTCCGTAAG	AACCTTCCAA	500
35	CAGGTCAGGC	TGGTGACAAC	GTAGGTCCTCC	TCCTTCGTGG	TATCGATAAAG	550
	GCTGAGGTAA	AGCGTGGTAT	GGTTGTTGTG	CACCCAGGTG	CTATTACTCC	600
	TCACGATCAC	TTCAAGGCAT	CTATCTATGT	ATTGAAGAAG	GAAGAGGGTG	650
	GTCGTCATAC	TCCATTGCGT	AACAAGTATC	GTCCACAGTT	CTACCTCCGT	700
40	ACAATGGACT	GTACAGGTGA	AATCCACCTC	CCAGAGGGCG	TTGAGATGGT	750
	TATGCCAGGT	GACAACGTAG	AGATTGAAGT	TGTATTGATC	TATAAGGTTG	800
	CTTTGAACGA	GGGTCTTCGT	T			821

45 2) INFORMATION FOR SEQ ID NO: 144

 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella oralis*
- (B) STRAIN: ATCC 33269

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60

	TGGTGCTATT	CTTGTAGTAG	CTGCTACTGA	CGGCCTATG	CCTCAAACTC	50
	GTGAACACGT	GCTTCTGCT	CGTCAGGTGA	ACGTACCTCG	TTGGTCGTT	100
	TTCTGAACA	AGTGCATAT	GGTTGACGAT	GAAGAAATGC	TTGAGCTCGT	150
5	AGAAATGGAG	CTTCATGAAC	TTCTCGAGCA	GTATGAATAT	GAGGAGGATA	200
	CTCCATTGT	TCGTGGTCG	GCACCTGGCG	CTCTGAATGG	AGTAGAGAAG	250
	TGGGTTGACA	GCGTGATGAA	GTTGATGGAT	ACCGTTGATG	AATGGATACA	300
	GGAACCACCG	CGTGATCTG	ATAAGCCTT	CTTGATGCCG	GTAGAGGATG	350
	TATTTTCTAT	TAATGGTCGT	GGAACGGTTG	TTACAGGCCG	TATTGAAACT	400
	GGTAAGGTTA	AGGTGGGCAG	TGAAGTTCAA	CTTCTTGGTC	TCGGTGAAGA	450
10	TAAGAAGTCC	GTTGTGACAG	GCCTTGAGAT	GTTCCGTAAG	ATTCTTGACG	500
	AAGGTGAAGC	TGGTGATAAT	GTAGGCTTGC	TGCTTCGTGG	TATCGATAAG	550
	ACGGAAGTAA	AGCGTGGTAT	GGTTGTCGTA	CATCCGGGGG	CTATTACTCC	600
	TCACGATCAT	TTCAAGGCTT	CAGTTACGT	ATTGAAGAAA	GAAGAAGGCG	650
	GTCGCCATAC	TCCGTTGGT	AMCAAGTATC	GTCCACAGTT	CTATCTTCGT	700
15	ACCATGGACT	GTACTGGTGA	AATTACTCTT	CCGGAAGGAG	TTGAGATGGT	750
	AATGCCGGGT	GATAACGTCG	AAATTGAAGT	TAAGTTGATC	TATCCGGTAG	800
	CTTTGAACGA	GGGACTTCGT	TTCGCTA			827

20

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Propionibacterium acnes*
- (B) STRAIN: ATCC 6919

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

	CGGCGCCATC	CTCGTGGTTG	CTGCTACCGA	CGGCCGATG	CCTCAGACTC	50
	GCGAGCACGT	TCTGCTCGCT	CGTCAGGTGG	GCGTGCCCGC	CATCGTCGTC	100
	GCCCTCAACA	AGTGCACAT	GGTTGACGAT	GAGGAGCTCA	TTGAGCTCGT	150
40	CGAGATGGAG	GTCCGCGAGC	TGCTGACCTC	GCAGGAGTTC	GACGGCGACA	200
	ACTGCCCTGT	CGTTCGCATC	TCCGCCCTCC	AGGCCCTCCA	GGGTGATGAG	250
	AAGTGGACCC	AGTCGATCCT	CGACCTCATG	GACGCCGTGG	ACGAGTACAT	300
	CCCGCAGCCT	GAGCGCGATC	TCGACAAGCC	CTTCCTTATG	CCGATCGAGG	350
	ACGTCTTCAC	CATCACCGGC	CGTGGCACCG	TTGTCACCGG	TCGTGTCGAG	400
45	CGCGCGTCG	TCAAGACTGG	CGAACAGGGTC	GAGATCGTCG	GTATCCACGA	450
	GAAGACCCAG	AAGACCAACCG	TTACCGGTGT	CGAGATGTC	CGCAAGATCC	500
	TCGACGGAGG	CCGCGCTGGT	GAGAACGTCG	CGCTTCTGCT	CCGTGGCAC	550
	AAGAAGGAGG	ATGTCGTTCG	CGGCATGGTC	CTCTCCAAGC	CTGTTCCAC	600
50	CACCCCCCAC	ACCGACCTCG	AGGGCCAGGT	CTACGTCCCTC	AAGAAGGATG	650
	AGGGTGGCCG	CCACAAGCCG	TTCTTCTCCC	ACTACAGCCC	CCAGTTCTAC	700
	TTCCGTACCA	CGGACGTGAC	TGGCACTGTT	GAGCTCCCCG	AGGGCACCAGA	750
	GATGGTCATG	CCTGGCGACA	ACACCGACAT	GACTGTGCAC	CTGATTCAAC	800
	CGGTTGCCAT	GGAGGATCAG	CTCAAGTTCG	CTA		833

55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: ATCC 35659

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGA	200
	GGCGAACGAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGAAT	TGACAAACCA	TTCCCTGTTAC	300
20	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
	CGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGGGAGA	ACGTAGGTTG	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAAGG	550
25	CTCAATCAAC	CCACACAAACA	AATTGAAATC	AGAAGTTTAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACCTGA	CGTAACGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAAACGT	GAACATGATC	GTTGA	745

30 2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
- (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
50	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGA	GGCGAACGAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGAAT	TGACAAACCA	TTCCCTGTTAC	CAATTGAGA	350
	CGTATTCTCA	ATTTCAAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAACCA	450
	ACAGCGAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTTG	TCTTCTGCGT	GGTACTAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAAGG	TTCAATCAAC	600
60	CCACACACTA	AATTGAAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACGTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG CGTAGAAATG	750
GTAATGCCAG GTGACAAACAT CAACATGATC GTTGAACGTGA TTCACCCAAAT	800
CGCGATGGAC GACGGTTAC GTTTCGCTA	829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC	50
GTGAGCACAT CCTGTTAGGT CGCCAGGTTG GTGTACCTTA CATCATCGTA	100
TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAACTGC TGGAATTAGT	150
AGAAATGGAA GTTCTGTGAAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG	200
ACACTCCAGT AATCCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT	250
GAGTGGGAAG CAAAAATTGT TGAATTAGCA GAAGCACTGG ATTCTTACAT	300
CCCAAAGAACCA GAGCGTGAA TTGACAAACC ATTCCGTGCTG CCTATCGAAG	350
30 ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTAGAG	400
CGTGGTGTGTTG TTAAAGTTGG TGAAGAAAGTT GAGATTGTTG GTATTAAAGA	450
CACAGTTAAA ACAACTTGTAA CTGGCGTTGA AATGTTCCGT AAATTACTTG	500
ACGAAGGTCCG TGCAGGTGAG AACGTAGGTG TTCTTCTGCG TGGTACTAAA	550
CGTGAAGAAA TCGAACGTGG ACAAGTACTG GCTAAACCAG GTTCAATCAA	600
35 GCCACACACT AAATTCGAAT CAGAAGTTA TATCCTGAGC AAAGATGAAG	650
GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC	700
CGTACAACGTG ACGTAACGTGG TACTATCGAA TTACCAAGAAG GCGTAGAAAT	750
GGTAATGCCA GGTGACAAACA TCAACATGAT CGTTGAACGTG ATTCAACCTA	800
TCGCGTAGGA CGACGGTTTA CGTT	824

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2) INFORMATION FOR SEQ ID NO: 149

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG TGAGCACATC CTGTTAGGTC GCCAAGTAGG TGTTCCCTTAC	50
60 ATCATCGTTT TCCTGAACAA ATGTGACATG GTAGACGACG AAGAACTGTT	100